

Qy	1	CAGGGGAAACCTGCAGCACTCAGAGACCTGGAATGGGTGAAAGCTGGAGGCTTCAGTGAAGAATA	60
Oy			
Db	1	CAGGTGAAATCTGCACCACTCAGACCTGGAATGGGTGAAAGCTGGAGGCTTCAGTGAAGAATA	60
Qy	61	TCTCTCAAGACTTCTGGANACAAATTGACCTGAATACACATGCACTTGGGTGAAGCAGAGC	120
Oy			
Db	61	TCTCTCAAGACTTCTGGANACAAATTGACCTGAATACACATGCACTTGGGTGAAGCAGAGC	120
Qy	121	CATGAAAAGAGCTTGAATGGATTGAGAGTTTAACTCTTAACAATGGTGTACTAACTAC	180
Oy			
Db	121	CATGAAAAGAGCTTGAATGGATTGAGAGTTTAACTCTTAACAATGGTGTACTAACTAC	180
Qy	181	AAGCAGAAGTTCAGAGGGCAGAGGCCAATTTGACTGTATACAAGTCTCCACACACAGGCTAC	240
Oy			
Db	181	AAGCAGAAGTTCAGAGGGCAGAGGCCAATTTGACTGTATACAAGTCTCCACACACAGGCTAC	240

QY 241 ATGAGCTCCGACCTGACATCTGAGGATTCTGACGTATTATCTGTGCAAGAGTACT 300
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Db 241 ATGAGCTCCGACCTGACATCTGAGGATTCTGACGTATTATCTGTGCAAGAGTACT 300
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|
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QY 301 ACCGTCCTGTTGCTTACTGAGTCCAAAGGACACCGGTCACTGCTCTCTCAGGTGAGGC 360
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|
|
Db 301 ACCGTCCTGTTGCTTACTGAGTCCAAAGGACACCGGTCACTGCTCTCTCAGGTGAGGC 360
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|
QY 361 GGTTCAGGCGGAGGTGGCTGTGGGGGTGGGAGATCGGACATCGAGCTCAGTCACTGCCA 420
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|
|
Db 361 GGTTCAGGCGGAGGTGGCTGTGGGGGTGGGAGATCGGACATCGAGCTCAGTCACTGCCA 420
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|
QY 421 GCAATCATGTCTGCATCTCCAGGGAGAGAGTCAACATACCTGACAGTGGCAGTCAAGT 480
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Db 421 GCAATCATGTCTGCATCTCCAGGGAGAGAGTCAACATACCTGACAGTGGCAGTCAAGT 480
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QY 481 ATAGTTACATGACCTGTACACAGACAGAGCTGTCACTTCCCAAAAGATGATTTAT 540
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|
|
Db 481 ATAGTTACATGACCTGTACACAGACAGAGCTGTCACTTCCCAAAAGATGATTTAT 540
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|
QY 541 GACACATCCAAACTGGCTTCTGAGTCCCTGCTGCTTCACTGAGTGGGCTGGGACC 600
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|
|
Db 541 GACACATCCAAACTGGCTTCTGAGTCCCTGCTGCTTCACTGAGTGGGCTGGGACC 600
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|
|
QY 601 TCTTATCTCTCACAATCAGCAGCATGAGGCTGTAGATGCTGCACCTTATTTATGTCAT 660
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|
Db 601 TCTTATCTCTCACAATCAGCAGCATGAGGCTGTAGATGCTGCACCTTATTTATGTCAT 660
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QY 661 CAGCGAGTATGTTACCCGCTCAGCTTGGTGTCTGGACACACAGTTGAAATTAACCG 717
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Db 661 CAGCGAGTATGTTACCCGCTCAGCTTGGTGTCTGGACACACAGTTGAAATTAACCG 717
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|
|

RESULT 2
AR231456
LOCUS AR231456 1176 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6451995.
ACCESSION AR231456
VERSION AR231456.1 GI:27272558
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1176)
AUTHORS Cheung,N.-K.V., Larsen,S.M., Guo,H.-F., Rivlin,K. and Sadetain,M.
TITLE Single chain Fv polynucleotide or peptide constructs of
anti-ganglioside GD2 antibodies, cells expressing same and related
methods
JOURNAL Patent: US 6451995-A 3 17-SEP-2002;
FEATURES
source Location/Qualifiers
1..1176
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ORIGIN
Query Match 99.7%; Score 715; DB 6; Length 1176;
Best Local Similarity 100.0%; Pred.No.4,1e-211;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTGAACTGCAGCAGTCAAGACTGAACTGGTGNAGCTTGAGGCTTCAGTGAAGATA 60
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Db 1 CAGGTGAACTGCAGCAGTCAAGACTGAACTGGTGNAGCTTGAGGCTTCAGTGAAGATA 60
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|
QY 61 TCTTCGCAAGACTTCTGAGAACAAATTCAGTAATACCAATGCACTGGGTGAAGCAGAGC 120
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Db 61 TCTTCGCAAGACTTCTGAGAACAAATTCAGTAATACCAATGCACTGGGTGAAGCAGAGC 120
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QY 121 CATGAAAGAGCCTTGAGTGAATTGAGATTATCTTAACAATGAGTGAATCTAATAC 180
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QY 181 AAGCAGAAATTCAAGGCGAAGCCACATTGACTGTAGACAAGTCTTCAGACACGCTAC 240
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Db 181 AAGCAGAAATTCAAGGCGAAGCCACATTGACTGTAGACAAGTCTTCAGACACGCTAC 240
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QY 241 ATGAGCTCCGACCTGACATCTGAGGATTCTGACGTATTATCTGTGCAAGAGTACT 300
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Db 241 ATGAGCTCCGACCTGACATCTGAGGATTCTGACGTATTATCTGTGCAAGAGTACT 300
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QY 301 ACCGTCCTGTTGCTTACTGAGTCCAAAGGACACCGGTCACTGCTCTCTCAGGTGAGGC 360
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|
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Db 301 ACCGTCCTGTTGCTTACTGAGTCCAAAGGACACCGGTCACTGCTCTCTCAGGTGAGGC 360
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QY 361 GGTTCAGGCGGAGGTGGCTGTGGGGGTGGGAGATCGGACATCGAGCTCAGTCACTGCCA 420
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|
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Db 361 GGTTCAGGCGGAGGTGGCTGTGGGGGTGGGAGATCGGACATCGAGCTCAGTCACTGCCA 420
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|
|
QY 421 GCAATCATGTCTGCATCTCCAGGGAGAGAGTCAACATACCTGACAGTGGCAGTCAAGT 480
|
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|
Db 421 GCAATCATGTCTGCATCTCCAGGGAGAGAGTCAACATACCTGACAGTGGCAGTCAAGT 480
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QY 481 ATAGTTACATGACCTGTACACAGACAGAGCTGTCACTTCCCAAAAGATGATTTAT 540
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QY 601 TCTTATCTCTCACAATCAGCAGCATGAGGCTGTAGATGCTGCCATTTATCTGCCAT 660
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Db 661 CAGCGAGTATGTTACCCGCTCAGCTTGGTGTCTGGACACACAGTTGAAATTAACCG 717
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RESULT 3
AR482235
LOCUS AR482235 717 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 5 from patent US 6703015.
ACCESSION AR482235
VERSION AR482235.1 GI:47244217
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 717)
AUTHORS Solomon,B. and Fienkel,D.
TITLE Filamentous bacteriophage displaying an .beta.-amyloid epitope
JOURNAL Patent: US 6703015-A 5 09-MAR-2004;
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 82.8%; Score 593.4; DB 6; Length 717;
Best Local Similarity 90.1%; Pred.No.3,2e-173;
Matches 646; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

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Db 1 CAGGTGAACTGCAGCAGTCAAGACTGAACTGGTGNAGCTTGAGGCTTCAGTGAAGATA 60
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|
|
QY 61 TCTTCGCAAGACTTCTGAGAACAAATTCAGTAATACCAATGCACTGGGTGAAGCAGAGC 120
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|
|
Db 61 TCTTCGCAAGACTTCTGAGAACAAATTCAGTAATACCAATGCACTGGGTGAAGCAGAGC 120
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|
|
QY 121 CATGAAAGAGCCTTGAGTGAATTGAGATTATCTTAACAATGAGTGAATCTAATAC 180
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Db 121 CATGAAAGAGCCTTGAGTGAATTGAGATTATCTTAACAATGAGTGAATCTAATAC 180
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QY 181 AAGCAGAAATTCAAGGCGAAGCCACATTGACTGTAGACAAGTCTTCAGACACGCTAC 240
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Db	Accession	Score	DB	Length	Match	Gap
Db	ATCAAAATTGAAGGCAAGCCACACTGATCTGTAGACAACTCCTCCACCACTCTACA	382				
Qy	242 TGAAGCTCCGAGCCTTGACATCTGAGATTCTGACGTCTATTACTGTGCAAGATACTA	301				
Db	383 TGCACTCAGAGCCTGACATCTGAGGACTCTGGGCTTATTACTGTGCAAGAAAGGACT	442				
Qy	382 CGGTCCGCTTGTCTTACTCTGGGTCCAAAGGAGACAGGTTCACCGTCTCCCTCAGGTGAGGCG	361				
Db	443 ATG---CTATGAGACTTACTGGGGCCCAAGGGACCAACGTCAACGTCCTCTCAGGTGAGTGC	499				
Qy	362 GTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATGTGGAACATGAGCTCACTCAGTCTCCAG	421				
Db	500 GTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATGTGGAACATGAGCTCACTCAGTCAACG	559				
Qy	422 CAATCATGTCTGCATCTTCAGAGGGAAGAAAGTCAACATGACCTGTGACGTGCCTCAAGTA	481				
Db	560 CAATCATGTCTGCATCTTCAGAGGGAAGAAAGTCAACATGACCTGTGACGTGCCTCAAGTA	619				
Qy	482 TAAATTACATGCACTGGTATCCAGCAGAAAGCTGTCACTCTCCCAAAAAGATGATTTATG	541				
Db	620 TAAATTACATGCACTGGTATCCAGCAGAAAGCTGTCACTCTCCCAAAAAGATGATTTATG	679				
Qy	542 AACATCCAACTGGCTCTTGGAGTCCCTGCTGCTTCAGTGGAGAGTGGGTCTGAGACT	601				
Db	660 AACATCCAACTGGCTCTTGGAGTCCCTGCTGCTTCAGTGGAGAGTGGGTCTGAGACT	739				
Qy	602 CTATTCTCTGCATCAGCAGCAGCATGAGGCTGTAGATGCTGCCACTTATTACTGCCATC	661				
Db	740 CTATTCTCTCTGCATCAGCAGCAGCATGAGGCTGTAGATGCTGCCACTTATTACTGCCATC	799				
Qy	662 AGCGGAGTATGTTACCCGCTCAGCTTCCGTGCTGTGGGACACAGTGTGGAATTAACGG	717				
Db	800 AGCGGAGTATGTTACCCAGTACGTTCGGTGTGAGGAGCAACAGCTGGAATTAACAGG	855				
RESULT 8						
AX839011	LOCUS	AX839011	716 bp	DNA	linear	PAT 15-DEC-2003
AX839011	DEFINITION	Sequence 1 from Patent WO03076465.				
AX839011	ACCESSION	AX839011				
AX839011.1	VERSION	GI:39922521				
KEYWORDS	SOURCE	synthetic construct				
ORGANISM	SOURCE	synthetic construct				
REFERENCE	SOURCE	other sequences; artificial sequences.				
AUTHORS	TITLE	Rancourt, C., Piche, A. and Beaudin, J. I.				
JOURNAL	TITLE	Downregulation of ca 125 tumor antigen and uses thereof				
FEATURES	LOCATION	Patent: WO 03076465-A 1 18-SEP-2003;				
FEATURES	LOCATION	Universite de Sherbrooke (CA)				
FEATURES	LOCATION	Location/Qualifiers				
FEATURES	LOCATION	1..716				
FEATURES	LOCATION	/organism="synthetic construct"				
FEATURES	LOCATION	/mol_type="unassigned DNA"				
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FEATURES	LOCATION	/note="VH-linker-VL portion of VK-8-1.9"				
ORIGIN						
Query Match	77.5%	Score 555.8	DB 6	Length 716		
Best Local Similarity	87.7%	Pred. No. 1.7e-161				
Matches 629	Conservative 0	Mismatches 84	Indels 4	Gaps 2		
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Qy	1	CAGGTGAATCTGCAGCAGTCAAGACTGTAATCTGTGTGNAAGCTTGGGGCTTCAGTGAAGTA	60			
Db	1	CAGGTCCAGCTGCAGAGTCAAGACTGTAATCTGTGAAAGCTTGGGGCTTCAGTGAAGTA	60			
Qy	61	TCCTGCAAG-CTTCGAGTACACATTCACGTACACAAATGACACTGGGTGAACAGAGC	119			
Db	61	TCCTGCAAGCTTGTGAMCAAAATTCATGATATACCATGACCTGAGGTGAACAGAGC	120			
Qy	121	CATGGAAGAGCTTGAAGTGTATGAGAGGATTTATTCCTTAACATGTGTGATCTTAATAC	180			
Db	120	CATGGAAGAGCTTGAAGTGTATGAGAGGATTTATTCCTTAACATGTGTGATCTGCTAC	179			

FEATURES	source
ORF	181 TAGCAGAGTCTCAAGGGGCAAGGCCACATTTGACTGTAGGCAAGTCTCCAGACAGAGCTTAC 240
ORF	180 AACCAAGAAATTTGAGGAACAAGGCGCTCTTTCAGTGTAGCACTTCTCCAGACAGAGCTTAC 239
ORF	241 ATGAGAGTCTCCCGAGGCTGACATCTTGAGGATTTCTGACAGCTATTAATCTGTGCAAGAGTACT 300
ORF	240 ATGAGAGTCTCCCGAGGCTGACATCTTGAGGAGCTCTGTGAGCTATTAATCTGTGCAAGAGTCTGG 299
ORF	301 ACGGTCCCG---TTTGCTTACTGGGTGCTCCAAAGGACCAACGAGTCAACCGTCTCTCCAGGTGGA 357
ORF	300 GGGTTTTTGTACTTGATGTCTGGGGGCAAGGGAGACCAAGTCAACCGTCTCTCCAGGTGGA 359
ORF	358 GGGCGTTTAAAGCGGAGAGGTGGCTCTTGGCGGTGGCGGATTTGAGCATCTGAGCTCACTCAAGTCT 417
ORF	360 GGGCGTTTAAAGCGGAGAGGTGGCTCTTGGCGGTGGCGGATTTGAGCATCTGAGATCAACCAAGTCT 419
ORF	418 CCAGCAATCATAGTCTGCATCTCCAGGGGAGAAAGTCACTATGATCCGTGAGTGGAGAGCTCA 477
ORF	420 CCAGCAATCTGCTGTGCAATCTCCAGGGGAGAAAGTCACAATGATCTTGGAGGGCCACCCCA 479
ORF	478 AGTATTAAGTTACATGCACTGTGTACAGAGCAAGCCTGTCAACCTCCCCCAAAAGATGATTT 537
ORF	480 AGTGAATTTACATGCACTGTGTATCAGAGAAAGCAAGATCTCTCCCCAAACCTTGATTT 539
ORF	538 TATGACACATCCAAATCGGCTTTCTGGAGTCCCTGCTGCTTCAGTGGAGGTGGGTCTGGG 597
ORF	540 TATACCAATCCAACTGGCTTTCTGGAGTCCCTGCTGCTTCAGTGGCGGTGGGTCTGGG 599
ORF	558 AACCCTTATTTCTCTCACAATCAGCAGCATGGAAGCTGTGAATGCTGTGCCACTTATTAATCTGC 657
ORF	600 AACCCTTATTTCTCTCACAATCAGCAGCATGGAAGCTGTGAATGCTGTGCCACTTATTAATCTGC 659
ORF	658 CATCAGCGGAGTAAAGTTAACCCGCTCACTGCTGGTGTGGGACACAGTTGGAAATATAA 714
ORF	660 CAGCAGTGGAGTCTGAGCCCAACCCACGTTCCGCTGTGGACCAAGCTGGAAATATAA 716
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RESULT 9	
LOCUS	AY374128 723 bp mRNA linear SYN 12-FEB-2004
DEFINITION	Synthetic construct anti-idiotypic B5 single chain variable
VERSION	AY374128
KEYWORDS	AY374128.1 GI:34979267
SOURCE	.
ORGANISM	synthetic construct
REFERENCE	synthetic construct
AUTHORS	other sequences; artificial sequences.
TITLE	1 (bases 1 to 723)
JOURNAL	Beninati,A., Arseni,S., Mancuso,G., Magliani,W., Conti,S.,
PUBMED	Midiri,A., Blondo,C., Polonelli,L. and Teti,G.
REFERENCE	Protective immunization against group B meningococci using
AUTHORS	anti-idiotypic mimics of the capsular polysaccharide
	J. Immunol. 172 (4), 2461-2468 (2004)
	14764718
	2 (bases 1 to 723)
	Beninati,A., Arseni,S., Mancuso,G., Magliani,W., Conti,S.,
	Midiri,A., Blondo,C., Polonelli,L. and Teti,G.
	Direct Submission
	Submitted (26-AUG-2003) Pathology and Experimental Microbiology,
	University of Messina, Via C. Valeria, 1 (Policlinico), Messina, Me
	I-98125, Italy
	Location/Qualifiers
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        /note="binds to anti-meningococcal Seam 3 monoclonal
        antibody; mimics immunogenic features of group B
        meningococcal polysaccharide"

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Query Match	76.7%	Score 550.2	DB 12	Length 723
Best Local Similarity	86.0%	Pred. No. 9.5e-160		
Matches 622	Conservative 0	Mismatches 95	Indels 6	Gaps 1

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YYCQQFTSPYTFGGGHHKEIKR"

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Query Match	76.7%	Score 550.2	DB 12	Length 723
Best Local Similarity	86.0%	Pred. No. 9.5e-160		
Matches 622	Conservative 0	Mismatches 95	Indels 6	Gaps 1
Qy	1	CAGGTGAAACTGCAAGCAGTCAAGACCTGAACTGTGTGAGCCGTGGGCTTCAGTGAAGATA	60	
Db	1	CAGGTGAAACTGCAAGCAGTCAAGACCTGAACTGTGTGAGCCGTGGGCTTCAGTGAAGATA	60	
Qy	61	TCCTGCAAGACTTGTGGAAACAAATTCACTGAATACCACTGCACTGGGTGAAGCAGAC	120	
Db	61	TCCTGCAAGACTTGTGGAAACAAATTCACTGAATACCACTGCACTGGGTGAAGCAGAC	120	
Qy	121	CATGGAAAGACCTTGAAGTGAATTTGAGGATTAATCTTAACAATGGTGTACTTAACCTAC	180	
Db	121	CCTGGGCAAGGACCTTGAAGTGAATTTGAGGATTAATCTTAACAATGGTGTACTTAACCTAC	180	
Qy	181	AAGCAGAAAGTTCAGAGGCAAGGCGACATTTGACTGTAGACAAAGTCTTCACAGACCTAC	240	
Db	181	AATAGAAAGTTCAAAGGCAAGGCGACATTTGACTGTAGACAAATCTTCACAGACCTAC	240	
Qy	241	ATGAGAGCTCCGACGCTGACATCTGAGGATTTCTGCACTTAATTAATCTGCAAGA-----	294	
Db	241	ATGAGAGCTCCGACGCTGACATCTGAGGATTTCTGCACTTAATTAATCTGCAAGA-----	294	
Qy	295	GATACCTACGGTCCGGTTGTGCTTACTGGGTCGAAGGAGCACAAGGTCACCGTCTCTCAGGT	354	
Db	301	AATTACTACAGAGCCCATGACTACTGGGGCCAGGACACACAGTCAACCTCTCAGGT	360	
Qy	355	GGAGGCGGTTCAAGGCGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGCTTCACTAG	414	
Db	361	GGAAGCGGTTCAAGGCGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGCTTCACTAG	420	
Qy	415	TCCTCAGCAATCAATGTCTGCATCTCCAGGGGAAAGTTCAACATGACTCTGAGTGGAGC	474	
Db	421	TCCTCAGCAATCAATGTCTGCATCTCCAGGGGAAAGTTCAACATGACTCTGAGTGGAGC	480	
Qy	475	TCAGGTAAAGTTACATGCACTGGTACACAGACGCTGTCACTCCCAAAAAGATGG	534	
Db	481	TCAGGTAAATTAATCACTGACTGTACACAGAAAGTCAAATGCTCTCCCAAAATGATGG	540	
Qy	535	ATTATGACACATCAAACTGGCTTCTGAGTCCCTGCTCGCTTCACTGAGCTGAGTCT	594	
Db	541	ATTATTAACATCAAACTGGCTCTGAGTCCCACTGCTTCACTGAGCTGAGTCT	600	
Qy	595	GGGACCTTATTTCTCCACAAATCAGAGAGATGAGGCTGTAGAATGTGCACTTAATAC	654	
Db	601	GGGAACTTATTTCTCCACAAATCAGAGAGATGAGGCTGTAGAATGTGCACTTAATAC	660	
Qy	655	TGCGCATCAGCGGAGTAGTAAACCGGCTCAGCTTGGTCTGGGACACAGTTGGAATAAAA	714	
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Qy	715	CGG 717		
Db	721	CGG 723		

DEFINITION Continuous in vitro evolution.
ACCESSION BD34870
VERSION BD34870.1 GI:33044640
KEYWORDS JP 2002515224-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 807)
AUTHORS Cota, G., Hudson, P.J., Iliades, P. and Irving, R.A.
TITLE Continuous in vitro evolution
JOURNAL Patent: JP 2002515224-A 4 28-MAY-2002;
DIATECH PTY LTD
OS Homo sapiens (human)
PN JP 2002515224-A/4
PD 28-MAY-2002
PF 07-MAY-1999 JP 2000548452
PR 08-MAY-1998 AU PP 3445
PI GREGORY COIA, PETER JOHN HUDSON, PETER ILIADES, ROBERT ALEXANDER
PI IRVING
PC C12N15/09, C12N15/01, C12P21/02, C12N15/00, C12N15/00 CC
Description of Sequence: Antihelipatitis surface antigen (4C2) CC
SCFV
FH Key Location/Qualifiers
FT source 1..807 /organism='Homo sapiens (human)'.
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source Location/Qualifiers
1..807 /organism='Homo sapiens'
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Query Match 76.4%; Score 547.6; DB 6; Length 807;
Best Local Similarity 85.2%; Pred. No. 6.2e-159;
Matches 610; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
QY 2 AGGTGAACCTGACAGACAGCTGAACTGAGTGGAGGCTTCACTGAAGATAT 61
DB 10 ATGTGAAGCTTCAGAGAGTCAGAGGCTGAGCTGGAGGCCCGGGGTCTCAGTGAAGATTA 69
QY 62 CCTCAAGACTTCTGAGAACAAATTCATCTGAATACACCATGACATGGGTGAAGAGACC 121
DB 70 CTGTCAAGGGTTCGGGCTACACATTCATCTGATATGCTATGCTATGGGTGAAGAGATC 129
QY 122 ATGGAAGAGCTTGAAGATTTGAGGTATTAATCTTAACATGTGTGTACTAATACA 181
DB 130 ATGCCAAGAGCTAGAGATTTGAGATTTAGTAATTCCTTGTGTAATCAAACTACA 189
QY 182 AGCGAAGTTCAGAGGCAAGGCCCATTTGATCTGAGACAGTCTCCAGCACACCTTACA 241
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QY 242 TGAAGCTCCGAGGCTGACATCTGAGATTTCTGAGTATTAATCTGTCAGAGATTA 301
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QY 362 GTTCAAGCGAGAGTGGCTCTGGGCGGTGGCGGATCGGACATGAGACTCACTAAGTCTCAG 421
DB 370 GTTCAAGCGAGAGTGGCTCTGGGCGGTGGCGGATCGGACATGAGACTCACTAAGTCTCAG 429
QY 422 CAATCATGTCGATCTCCAGGGAAGAGTCAACATGACCTGAGAGTGGAGCTCAAGTA 481
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QY 542 ACACATCCAAACTGGCTTCTGAGTCCCTGCTCGCTTCAAGTGAAGTGGTCTGGAGACT 601
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DB 610 CTCACCTCTTCACAAATGACAGACAGTGGAGGCTGAAATGCTGCCACTTATTAATCTCCATC 669
QY 662 AGCGAGTATGATACCCGCTCACTGCTGGTGTGGAGACAGAGTGGAAATTAAGG 717
DB 670 ACTGAGATGATGATACCTCCACGTTCCGTTGGTGGAGACCAAGCTGAAATTAAGG 725
RESULT 11
AR317194
LOCUS AR317194 807 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 4 from patent US 6562622.
ACCESSION AR317194
VERSION AR317194.1 GI:33696534
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 807)
AUTHORS Cota, G., Hudson, P.J., Iliades, P. and Irving, R.A.
TITLE Continuous in vitro evolution
JOURNAL Patent: US 6562622-A 4 13-MAY-2003;
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Query Match 76.4%; Score 547.6; DB 6; Length 807;
Best Local Similarity 85.2%; Pred. No. 6.2e-159;
Matches 610; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
QY 2 AGGTGAACCTGACAGACAGCTGAACTGAGTGGAGGCTTCACTGAAGATAT 61
DB 10 ATGTGAAGCTTCAGAGAGTCAGAGGCTGAGCTGGAGGCCCGGGGTCTCAGTGAAGATTA 69
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DB 70 CTGTCAAGGGTTCGGGCTACACATTCATCTGATATGCTATGCTATGGGTGAAGAGATC 129
QY 122 ATGGAAGAGCTTGAAGATTTGAGGTATTAATCTTAACATGTGTGTACTAATACA 181
DB 130 ATGCCAAGAGCTAGAGATTTGAGATTTAGTAATTCCTTGTGTAATCAAACTACA 189
QY 182 AGCGAAGTTCAGAGGCAAGGCCCATTTGATCTGAGACAGTCTCCAGCACACCTTACA 241
DB 190 ACCGAAGTTCAGAGGCAAGGCCCATTTGATCTGAGACAGTCTCCAGCACAGCTATT 249
QY 242 TGAAGCTCCGAGGCTGACATCTGAGATTTCTGAGTATTAATCTGTCAGAGATTA 301
DB 250 TGAAGCTTGGCAGATTTGACATCTGAGATTTCTGCAATCTATTAATCTGTCAGAGATTC 309
QY 302 CGGTCCGTTTGTCTTACTGAGTTCAGAGGACCAAGGTCAAGCTCTCTCAGAGTGAAGCG 361
DB 310 ACTGATCTTCGATGATCTGAGGCGCAAGGACCAAGGTCAAGCTCTCTCAGAGTGAAGCG 369
QY 362 GTTCAAGCGAGAGTGGCTCTGGGCGGTGGCGGATCGGACATGAGACTCACTAAGTCTCAG 421
DB 370 GTTCAAGCGAGAGTGGCTCTGGGCGGTGGCGGATCGGACATGAGACTCACTAAGTCTCAG 429
QY 422 CAATCATGTCGATCTCCAGGGAAGAGTCAACATGACCTGAGAGTGGAGCTCAAGTA 481
DB 430 CAATCATGTCGATCTCCAGGGAAGAGTCAACATGACCTGAGAGTGGAGCTCAAGTA 489
QY 482 TAAATTACATGACATGTGTACAGAGAGAGCTGTCACTCCCAAAAGATGATTTATG 541
DB 490 TCAGTACGTCATCTGTATCAACAGAGAGTCAAGGACCTCCCAAAAGATGATTTATG 549

Oy	542	ACACATCCAACTGGCTTCGAGATCCCTCGTGCCTTCAGTGAGGAGGTCTGGACA	601
Dd	550	AACAATCCAACTGGCTTCGAGATCCCTCGTGCCTTCAGTGAGGAGGTCTGGACA	609
Oy	602	CTTATTCTCACAATCAGCAGCATGAGAGCTGTAGATGCTGCCATTACTGCCATC	661
Dd	610	CTCACTCTCACAATCAGCAGCTTTGAAGAGCTGAAGAATGCTGCCATTACTGCCAGC	669
Oy	662	AGCGAGTAGTTACCCGCTCACGTTCCGCTGCTGGACACAGTTGGAAATAAACC	717
Dd	670	ACTGGAGTAGTAACCCCTCCACAGTTCGCTGGGACCAAGCTGAAATAAACC	725
RESULT 12			
LOCUS	AF189283	1815 bp mRNA linear SYN 23-MAR-2000	
DEFINITION		Synthetic construct chimeric single chain fragment variable antibody 10B5 scFv mRNA, complete cds.	
ACCESSION	AF189283		
VERSION	AF189283.1	GI:7230485	
KEYWORDS			
SOURCE		synthetic construct	
ORGANISM		synthetic construct	
REFERENCE		other sequences; artificial sequences.	
AUTHORS		1 (bases 1 to 1815)	
TITLE		Long, M.C., Unger, S., Mah, D.C., Jubailey, L., Mah, M.A., Masri, S.A. and Nagata, L.P.	
JOURNAL		Construction and characterization of a novel recombinant single-chain variable fragment antibody against Western equine encephalitis virus	
MEDLINE		Hybridoma 19 (1), 1-13 (2000)	
PUBMED		20229323	
REFERENCE		10768836	
AUTHORS		2 (bases 1 to 1815)	
TITLE		Long, M.C., Unger, S., Mah, D.C.W., Jubailey, L., Mah, M.A., Masri, S.A. and Nagata, L.P.	
JOURNAL		Direct Submission	
FEATURES		Submitted (23-Sep-1999) Medical Countermeasures Section, Defence Research Establishment Suffield, P.O. Box 4000, Station Main, Medicine Hat, Alberta T1A 8K6, Canada	
Source		Location/Qualifiers	
CDS		1..1815	
		/organism="synthetic construct"	
		/mol_type="mRNA"	
		/db_xref="taxon:32630"	
		/cell_line="hybridoma expressing a monoclonal antibody that recognizes Western equine encephalomyelitis virus"	
		1..1815	
		/note="chimeric single chain fragment variable (scFv) antibody fused to the human heavy chain immunoglobulin gamma 1 constant domains (CH1-CH3; A 6 His tag and an enterokinase recognition site is present at the N-terminal end of the protein"	
		/codon_start=1	
		/transl_table=11	
		/product="10B5_scFv"	
		/protein_id="AAF42993.1"	
		/db_xref="GI:7230486"	
		/translation="MRSGHHNHGHMAEMTGQGMGRDLYDDDKRWKSELETCSWYHGIPLVFPYAQPAMADVKIQQSASLEVKRTSVKASCXASGNFTSYIWNKLARKGQGLIEWIDIPVGSSTINYNEKRFPSKALLIVDTSSITAYMQLSLASDLSALYYICARGDYGSFFDWGQGVTVTVSSGGSGSGSGSGSPIDLTQSPAIMASPGKKVITCSVSSITSSENLMHYOOKSETSPKPWIYGTSNLASGVVPFSGGSTYSLLTISMEAEAPDAATYYCOORSSYLPTFGAGRKLTKRAAGCLVDYPPEVPTYSMNNGALTSGVHTFRPAVLOSGLYSLASSVTYTPSSSLTGCTGYICNVNKRPSTKYDKVEPESCKTKCPBPCEAPLILGPSVFPLPPPKRDTLMIKRPEVTCVVVDSDHDEPKENMYDVGVENAKTRKREQYNSTRKAVSVLTIVLDQMWDNGEKYCKVNKAFLPATETTKISKAGQEPKEPOVTLTPPRDELTKNQVSLTCLVKGFYPSDIAVMESNGQPENNYKTTPPVLDSDGSEFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTHKA"	
		175..9132	
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		913..1812	
		/note="Region: human IgG1 Fc"	
		misc_feature	
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Query Match	76.2%	Score 546;	DB 12;	Length 1815;
Best Local Similarity	87.2%	Pred. No. 2e-158;		
Matches 633;	Conservative 1;	Mismatches 83;	Indels 9;	Gaps 3;
QY 1	CAGGGAACCTGCGACGAGTCAAGACCTGAACTGGTGNAGCCTGGGGCTTCAGTGAATATA	60		
DB 184	CAGGTCAAGCTGCGACAGTCTGGAGCTGAGCTTGTGAAGCTGGGACTTCAGTGAACCTG	243		
QY 61	TCCTGCAAGACTTCTGGANACAAATTCAGTAATACATGCACTGGGTGAACAGAGC	120		
DB 244	TCCTGCAAGAGCTTCTGGCTACAACTTCACAGCACTGATTAACCTGGGTGAAGCTGAGG	303		
QY 121	CATGAAAGAGCCTTGTAGTGGATTGGAGGATTAATCTTAACAATGGTGGTACTAATAC	180		
DB 304	CCTGACCAAGGCTTGTAGTGGATTGGAGATTAATTAATCTGGTGGTGGTGGTGGTGGTGG	363		
QY 181	AAGCAAGAGTTCAGAGGCAAGGCAAGGCAATGTCGTGTAGCAAGTCTTCAGACAGCTAC	240		
DB 364	AATGAGAGTTCAG	423		
QY 241	ATGAGAGCTCCGACAGCTGACATCTGAGAGATTCGACATTAATTAATCTGCAAGA -GATAC	299		
DB 424	ATGCAACTCAAGCAAGCTGGAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	483		
QY 300	TACGGT - CCGCTTGTCTTACTGGGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	357		
DB 484	TACGGTGTAGTACTTGTACTACTGGGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	543		
QY 358	GCGGTTCAAGGCGAG	417		
DB 544	GCGGTTCAAGGCGAG	603		
QY 418	CCAGCAATCATGTCTGACATCTCCAGGGGAGAGAGTCAACATGACCTGAGTGGAGCTCA	477		
DB 604	CCAGCAATCATGTGACAGATCTCCAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	663		
QY 478	AGTATAGT-----ACATGCACTGTGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	531		
DB 664	AGTATAGTGTCCAGCACTGT	723		
QY 532	TGAGTTTATGACATCCAACTGGGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	591		
DB 724	TGAGTTTATGACATCCAACTGGGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	783		
QY 592	TCTGGGAGCTTATTTCTCTCACATCAGCAGTGGAGCTGTAGATGTCTGCACATTAT	651		
DB 784	TCTGGGAGCTTATTTCTCTCACATCAGCAGTGGAGCTGTAGATGTCTGCACATTAT	843		
QY 652	TACTGCCATCAGCGAGAGTGAATCCCGCTCAAGTTCGGTGTGGAGACAGTGGAAATA	711		
DB 844	TACTGTCAACAGAGAGAGTGAATCCCGCTCAAGTTCGGAGCTGGAGACAAAGTGGAAATA	903		
QY 712	AAACGG 717			
DB 904	AAACGG 909			
RESULT 13				
A97142				
LOCUS	A97142	725 bp	DNA	linear
DEFINITION	Sequence 8 from Patent WO9191361.			
ACCESSION	A97142			
VERSION	A97142.1	GI:6780530		
KEYWORDS				
SOURCE	Mus sp.			
ORGANISM	Mus sp.			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
TITLE	1 (bases 1 to 725)			
	Petril, H. and Bosslet, K.			
	BONDING MOLECULES AGAINST RECEPTOR-LIGAND-COMPLEXES			

JOURNAL Patent: WO 9919361-A 8 22-APR-1999;
PETRUL HEIKR (CA); BOSSLET KLAUS (US)
FEATURES Location/Qualifiers
Source 1..725
/organism="Mus sp."

/mol_type="unassigned DNA"
/db_xref="taxon:10095"
/issue_type="WILZ"

ORIGIN

Query Match 75.5%; Score 541.4; DB 6; Length 725;
Best Local Similarity 85.8%; Pred. No. 5.2e-157;
Matches 612; Conservative 0; Mismatches 98; Indels 3; Gaps 1;

QY 8 AACTGCACAGCTCAGAGCTGAACTGAGGCTTGGGCTTCAATGAAATATCTTCA 67
DB 13 AAGCTCAGACGATCAGACCTGAACTGAGAGCCCTGGGCTTGGTGAAGATGTCCTCA 72
QY 68 AGACTTCTGAGAACAAATTCCTGAATACACATGACATGGGCTGAAGAGAGCATGGA 127
DB 73 AGGCTTCTGAGATCAGATTCAGTCACTAGCTATGTTATTCCTGGTGAAGAGAGACTGAGC 132
QY 128 AGAGCTTGAAGTGAATGAGGATTAATTCCTAACATGATGATCTAATACTACAGAGA 187
DB 133 AGGGCTTGAAGTGAATGAGGATTAATTCCTGAAGTGAATTAATTAATACTACAGAGA 192
QY 188 AGTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 247
DB 193 AGTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 252
QY 248 TCCGAGGCTGACATCTGAGGATTCCTGAGTCTATTAATCTGAGGAGGAGGAGGAGGAGG 307
DB 253 TCAGAGGCTGACATCTGAGGATTCCTGAGTCTATTAATCTGAGGAGGAGGAGGAGGAGG 312
QY 308 C-----TTTGTCTTACTGAGGATTCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 364
DB 313 GGTACTTGAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 372
QY 365 CAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 424
DB 373 CAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 432
QY 425 TCATGTCGACATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 484
DB 433 TCATGTCGACATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 492
QY 485 GTTACATGACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 544
DB 493 GTTACATGACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 552
QY 545 CATCAAACTGAGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 604
DB 553 CATCAAACTGAGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 612
QY 605 ATTCTCTCAGATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 664
DB 613 ATTCTCTCAGATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 672
QY 665 GAGAGTGAATCCCGCTCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 717
DB 673 GAGAGTGAATCCCGCTCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 725

RESULT 14
LOCUS CQ768808 811 bp DNA linear PAT 04-MAR-2004
DEFINITION Sequence 27 from Patent WO2004007550.
ACCESSION CQ768808
VERSION CQ768808.1 GI:45112092
KEYWORDS
SOURCE
ORGANISM
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Unger C.M., Zehetmeier C., Torella C., Niewoehner J., Ahrens B. and
Beese G.
TITLE Mcam inhibitors
JOURNAL Patent: WO 2004007550-A 27 22-JAN-2004;
Xerion Pharmaceuticals GmbH (DE)
FEATURES Location/Qualifiers
Source 1..811
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: scFv"

ORIGIN

Query Match 75.2%; Score 539.2; DB 6; Length 811;
Best Local Similarity 86.2%; Pred. No. 2.6e-156;
Matches 624; Conservative 0; Mismatches 85; Indels 15; Gaps 2;

QY 6 GAACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 65
DB 1 GAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
QY 66 CAAAGCTTCTGAGAACAAATTCAGTGAATACCATGACATGAGGAGGAGGAGGAGGAGGAGG 125
DB 61 CAAAGCTTCTGAGAACAAATTCAGTGAATACCATGACATGAGGAGGAGGAGGAGGAGGAGG 120
QY 126 AAAGAGCTTGAAGTGAATGAGGATTAATCTTCAACATGATGATGATGATGATGATGAT 185
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QY 186 GAAAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 245
DB 181 GAAAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
QY 246 GCTCCGAGGCTGACATCTGAGGATTCCTGAGTCTATTAATCTGAGGAGGAGGAGGAGGAGG 296
DB 241 GCTCCGAGGCTGACATCTGAGGATTCCTGAGTCTATTAATCTGAGGAGGAGGAGGAGGAGG 300
QY 297 TACTAGGATCCCGTTTGTCTTACTGAGGATTCCTGAGGAGGAGGAGGAGGAGGAGGAGG 356
DB 301 CGTGGCGGTGATCTTCAATGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
QY 357 AGGCGGTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 410
DB 361 AGGCGGTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
QY 411 TCAGTCTCAGACATCAATGATGATCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 470
DB 421 CCAATCTCAGACATCAATGATGATCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
QY 471 CAGCTCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 530
DB 481 CAGCTCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 531 ATGATTTTGAAGACATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 590
DB 541 ATGATTTTGAAGACATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 591 GTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 650
DB 601 GTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 651 TTAATGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 710
DB 661 TTAATGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
QY 711 AAAA 714
DB 721 GAAA 724

RESULT 15
CQ802042

LOCUS CO802042 811 bp DNA linear PAT 05-MAY-2004
DEFINITION Sequence 27 from Patent WO2004007717.
ACCESSION CO802042
VERSION CO802042.1 GI:47058596
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Unger, C.M., Beate, G., Jensen, K.H., Zehetmeier, C., Krauer, R.,
Guelbenzu, B.L., Torella, C. and Ilag, L.L.
TITLE Proteomic screen to identify disease-related biological
JOURNAL molecules and inhibitors thereto
Patent: WO 2004007717-A 27 22-JAN-2004;
Xerion Pharmaceuticals AG (DE)
FEATURES
Source Location/Qualifiers
1. 811
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: scFv"

ORIGIN
Query Match 75.2%; Score 539.2; DB 6; Length 811;
Best Local Similarity 86.2%; Pred. No. 2.6e-156;
Matches 624; Conservative 0; Mismatches 85; Indels 15; Gaps 2;

QY 6 GAAATCTGACAGCTCAGGACCTGACCTGAGGAGCTTGGGGCTTCACTGAGTAAATATCTCTG 65
DB 1 GCAGCTGAAGAGAGCAGACCTGAGCTGTGAACCTGGGGCTTCACTGAGTAAATATCTCTG 60
QY 66 CAAGACTTCTGGANACAAATTTCACTGAATACACATGACCTGGGGTGAAGCAGAGCCATGG 125
DB 61 CAAGGCTTCTGGATACATTTCACTGACCTGACATGACCTGGGGTGAAGCAGAGCCATGG 120
QY 126 AAAAGGCTTGAAGTGAATGAGGATTAATCTTAACATGAGTGAATTAATCAACAACA 185
DB 121 AAAGAGCTTGAAGTGAATGAGGATTAATCTTAACATGAGTGAATTAATCAACAACA 180
QY 186 GAAGTTGAAGGAGCAGAGCCATTTGATGATGACCAAGTCTTCCAGCAGAGCTTACATGA 245
DB 181 GAAGTTGAAGCAGAGCCATTTGATGATGACCAAGTCTTCCAGCAGAGCTTACATGA 240
QY 246 GCTCCGAGGCTGACATCTGAGGATTTGAGGATTTGAGGATTTGAGGATTTGAGGATTTG 296
DB 241 GCTCCGAGGCTGACATCTGAGGATTTGAGGATTTGAGGATTTGAGGATTTGAGGATTTG 300
QY 297 TACTACGCTCCGTTTGTCTTAATGAGGATTTGAGGATTTGAGGATTTGAGGATTTGAGG 356
DB 301 CGTGGCGTGGTACTTGCATGCTGGGGGCGAGGAGCAGGATCAGGATCAGGATCAGGAT 360
QY 357 AGGCGGTTCAAGGAGGAGTGGCTTGGCGGTGGCGGATCGG-----ACATCGAGCTCAC 410
DB 361 AGGCGGTTCAAGGAGGAGTGGCTTGGCGGTGGCGGATCGG-----ACATCGAGCTCAC 420
QY 411 TCACTCCAGCATCATGCTGATCTCCAGGGGAGAGATGACCATGACCTGAGTGG 470
DB 421 CCACTCCAGCATCATGAGTCTTGGGGGCAAAAGTCAACATCACTGCACTGC 480
QY 471 CAGCTCAAGTATAAGTTACATGCACTGTGTACCAAGAGCCTGTCACTTCCCAAAAG 530
DB 481 CAGCTCAAGTATAAGTTACATGCACTGTGTACCAAGAGCCTGTCCCAAAAG 540
QY 531 ATGATTTATGACATCCAACTGGCTTTCGAGTCCCTGCTGCTTCACTGAGTGG 590
DB 541 ATGATTTATGACATCCAACTGGCTTTCGAGTCCCTGCTGCTTCACTGAGTGG 600
QY 591 GTCTGGAGCCTTATTTCTCTCAATCAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 650
DB 601 GTCTGGAGCCTTATTTCTCTCAATCAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 651 TTACTGCCATCAGGAGGAGTACCCGCTCAGCTTGGCTGGGACACAGTTGGAAT 710

DB 661 TTACTGCCAGAGTGGAGTGAATACCACTCACTTGGTGGTGGAGCAGAGCTGGAGCT 720
QY 711 AAAA 714
DB 721 GAAA 724

Search completed: February 18, 2005, 22:25:56
Job time : 3234.76 secs

CC melanomas and small cell lung cancer. The peptide can be detectably
CC labelled, preferably with 99m-Tc, for tissue imaging of cells expressing
CC GD2. It can also be used to target delivery of a therapeutic or pre-
CC therapeutic agent, such as a toxin, streptavidin or a pro-drug converting
CC enzyme, to cells expressing GD2. The peptide may further comprise CD8 to
CC facilitate the formation of GD2-targeted lymphocytes. T cells containing
CC the peptide can also be used to target GD2-producing tumour cells
XX

SO Sequence 717 BP; 180 A; 181 C; 195 G; 159 T; 0 U; 2 Other;

Query Match 99.7%; Score 715; DB 2; Length 717;
Best Local Similarity 100.0%; Pred. No. 1.1e-192;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CAGGTGAAACTGCGACGAGTCTGAGACCTGAACTGGTGNAGCGCTGGGGCTTGAGTGAAGATA 60
D 1 CAGGTGAAACTGCGACGAGTCTGAGACCTGAACTGGTGNAGCGCTGGGGCTTGAGTGAAGATA 60
QY 61 TCCTGCAAGACTTCTGAGAACAAATTCATGTAATACATGCACTGGGTGAAGCAGAGC 120
D 61 TCCTGCAAGACTTCTGAGAACAAATTCATGTAATACATGCACTGGGTGAAGCAGAGC 120
QY 121 CATGGAAGAGCCTTGAGTGGATTGAGATTATCTTAACAATGGTGTACTACTAC 180
D 121 CATGGAAGAGCCTTGAGTGGATTGAGATTATCTTAACAATGGTGTACTACTAC 180
QY 181 AAGCAGAGTTCAAGGGCAAGGCCACATGACTGTAGACAAGTCTGCACACAGCCTAC 240
D 181 AAGCAGAGTTCAAGGGCAAGGCCACATGACTGTAGACAAGTCTGCACACAGCCTAC 240
QY 241 ATGAGAGTCCGACGCTGACATCTGAGATTCTGCACTATTACTGTGCAAGAGTACT 300
D 241 ATGAGAGTCCGACGCTGACATCTGAGATTCTGCACTATTACTGTGCAAGAGTACT 300
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D 301 ACGGTCCCGTTTGTACTGGTCTCAAGGGACACCGTCCCTCTCTCAAGTGAAGCC 360
QY 361 GGTTCCAGGCGAGGTGCTCTGGGCGGTGGGCGATCGGACATCGACATCGACTCACTGCCA 420
D 361 GGTTCCAGGCGAGGTGCTCTGGGCGGTGGGCGATCGGACATCGACATCGACTCACTGCCA 420
QY 421 GCAATCATGTCGTGATCTCCAGGGGAGAAAGTCACTGACCTGCACTGAGTCAAGT 480
D 421 GCAATCATGTCGTGATCTCCAGGGGAGAAAGTCACTGACCTGCACTGAGTCAAGT 480
QY 481 ATAGATTACATGCACTGTAACACAGACAGCCTGTCACTCCCAAAAAGATGATTAT 540
D 481 ATAGATTACATGCACTGTAACACAGACAGCCTGTCACTCCCAAAAAGATGATTAT 540
QY 541 GACACATCCAAACTGGCTTCTGAGAGTCCGTGCTCGCTTCAGTGGCAGTGGGTCTGGAGCC 600
D 541 GACACATCCAAACTGGCTTCTGAGAGTCCGTGCTCGCTTCAGTGGCAGTGGGTCTGGAGCC 600
QY 601 TCTTATTTCTGCAATCAGCAGCATGAGAGCTGTAGTANTCTGCACTTATTTACTGCGAT 660
D 601 TCTTATTTCTGCAATCAGCAGCATGAGAGCTGTAGTANTCTGCACTTATTTACTGCGAT 660
QY 661 CACGGAGAGTATTACCGGCTCAGCTTGGTGGTGGGACACAGTTGGAAAATTAACGG 717
D 661 CACGGAGAGTATTACCGGCTCAGCTTGGTGGTGGGACACAGTTGGAAAATTAACGG 717
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RESULT 2

ABA92026
ID ABA92026 standard; cDNA; 717 BP.

AC ABA92026;

XX 23-MAY-2002 (first entry)

DE Anti-disialoganglioside GD2 single chain antibody 5F11 scFv cDNA.

KM Single chain antibody; scFv; antibody; disialoganglioside GD2;
KW antitumour; immunostimulant; neuroblastoma; melanoma; sarcoma;
XX small lung carcinoma; brain tumour; cancer; therapy; imaging; gene; ss.

OS Mus sp.

PN US002018783-A1.

PD 14-FEB-2002.

PF 30-SEP-1997; 97US-00940544.

PR 20-MAR-1997; 97WO-US004427.

PA (SADÉ/) SADELAIN M.

PA (CHEN/) CHENG N V.

PA (KRAU/) KRAUSE A.

PA (GUOH/) GUO H.

PI Sadelain M, Cheung NV, Krause A, Guo H;

DR WPI; 2002-239251/29.

PS Disclosure; Page 3; 9pp; English.

CC The present sequence is that of cDNA encoding a single chain scFv
CC antibody that is derived from an anti-disialoganglioside GD2 antibody
CC produced by 5F11 hybridoma cells. The scFv comprises the 5F11 variable
CC chains in VH-VL orientation. mRNA from 5F11 hybridoma cells was used in
CC the construction of the present 5F11 scFv gene using a mouse scFv
CC module/recombinant phage antibody system. The scFv can be used in fusion
CC proteins of the invention which comprise an scFv antibody linked to the
CC human T cell surface receptor CD28. T cells expressing such fusion
CC proteins exhibit enhanced survival when reintroduced to an in vivo
CC environment. They can be used to induce an immune response to cells that
CC express the antigen to which the antibody is specific. Cells expressing a
CC fusion protein including an anti-GD2 scFv are useful for treatment of
CC melanomas, neuroblastomas, small lung carcinoma, sarcomas and brain
CC tumours that express GD2 as a surface antigen. Cells expressing the
CC fusion proteins of the invention can also be used for in vitro purging of
CC stem cells or bone marrow and for in vivo targeting of tumour cells and
CC other antigen-bearing cells for imaging

SO Sequence 717 BP; 180 A; 181 C; 195 G; 159 T; 0 U; 2 Other;

Query Match 99.7%; Score 715; DB 6; Length 717;
Best Local Similarity 100.0%; Pred. No. 1.1e-192;

Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CAGGTGAAACTGCGACGAGTCTGAGACCTGAACTGGTGNAGCGCTGGGGCTTGAGTGAAGATA 60
D 1 CAGGTGAAACTGCGACGAGTCTGAGACCTGAACTGGTGNAGCGCTGGGGCTTGAGTGAAGATA 60
QY 61 TCCTGCAAGACTTCTGAGAACAAATTCATGTAATACATGCACTGGGTGAAGCAGAGC 120
D 61 TCCTGCAAGACTTCTGAGAACAAATTCATGTAATACATGCACTGGGTGAAGCAGAGC 120
QY 121 CATGGAAGAGCCTTGAGTGGATTGAGATTATCTTAACAATGGTGTACTACTAC 180
D 121 CATGGAAGAGCCTTGAGTGGATTGAGATTATCTTAACAATGGTGTACTACTAC 180
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D 181 AAGCAGAGTTCAAGGGCAAGGCCACATGACTGTAGACAAGTCTGCACACAGCCTAC 240
QY 241 ATGAGAGTCCGACGCTGACATCTGAGATTCTGCACTATTACTGTGCAAGAGTACT 300
D 241 ATGAGAGTCCGACGCTGACATCTGAGATTCTGCACTATTACTGTGCAAGAGTACT 300
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RESULT 4
 ID AAC85539 standard; DNA, 717 BP.
 AC AAC85539;
 XX
 DT 04-JUN-2001 (first entry)
 XX
 DE scFv 508F coding sequence.
 XX
 KW Human; prion protein; plaque forming disease; display vehicle; kuru;
 KW aggregating protein; amyloid plaque; brain; early onset; senility;
 KW Alzheimer's disease; late onset; pre-symptomatic; SAA amyloidosis;
 KW hereditary Icelandic syndrome; multiple myeloma; scrapie; BSE; CJD;
 KW bovine spongiform encephalopathy; Creutzfeldt-Jakob Disease; FPI;
 KW Gerstmann-Strausler-Sheinker Disease; GSS; fatal familial insomnia;
 KW antibody; ss.
 XX
 OS Synthetic.
 XX
 PN WO200118169-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 31-AUG-2000; 2000WO-IL000518.
 XX
 PR 03-SEP-1999; 99US-0152417P.
 PR 29-DEC-1999; 99US-00473653.
 PR 31-JUL-2000; 2000US-00629971.
 XX
 PA (UTRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
 XX
 PI Solomon B, Frenkel D, Hanan E;
 DR P-P8DB; AAB47111.
 XX
 PT Treating amyloidogenic disease such as Alzheimer's disease, BSE or CJD
 PT comprises presentation of plaque derived antigens or epitopes on a
 PT display vehicle, and introducing the vehicle into the recipient.
 XX
 PS Example 2; Fig 11; 120pp; English.
 XX
 CC This sequence encodes scFv 508F heavy chain, linker and light chain. The
 CC scFv fragment was derived from the 508 IGM hybridoma which is generated
 CC from splenocytes of a mouse that has been immunised with a peptide
 CC corresponding to the 16 amino terminal residues of beta-A β conjugated to
 CC keyhole limpet hemocyanin used a carrier. The resultant variable chain
 CC fragments may be used in the method of the invention. Cys 96 of the VL
 CC fragment was replaced with various amino acids to see if production yield
 CC or stability were effected without having an adverse effect on its
 CC binding affinity. The invention provides an agent for treating a plaque
 CC forming disease. Antigenic polypeptides are displayed on a display
 CC vehicle and are capable of eliciting antibodies capable of disaggregating
 CC the aggregating protein and/or of preventing aggregation of the
 CC aggregating protein. This reduces formation of amyloid plaques in the
 CC brain of victims of plaque forming diseases, e.g. early onset Alzheimer's
 CC disease, late onset Alzheimer's disease, pre-symptomatic Alzheimer's
 CC disease, SAA amyloidosis, hereditary Icelandic syndrome, senility,
 CC multiple myeloma, scrapie, bovine spongiform encephalopathy (BSE), kuru,
 CC Creutzfeldt-Jakob Disease (CJD), Gerstmann-Strausler-Sheinker Disease
 CC (GSS) and fatal familial insomnia (FPI)
 CC
 SO Sequence 717 BP, 178 A; 174 C; 198 G; 167 T; 0 U; 0 Other;
 Query Match 82.8%; Score 593.4; DB 4; Length 717;
 Best Local Similarity 90.1%; Pred. NO. 4e-158;
 Matches 646; Conservative 0; Mismatches 66; Indels 3; Gaps 1,1;
 1 CAGGTGAACCTGACAGCTGACGACCTGAACTGATGCTGGGGCTTCAGTGAAGATA 60

Db	1	CAGGTCCAAACTGCAAGAGTCAAGGGGCTAGCTGTGTGAGGCGCTGGGGTCTCACTGAAGAATT	60
Qy	61	TCCTGCAAGACTTGTGAMACAAATTCCTGAATAACCAATGACACTGGGTGAAGCAGAC	120
Db	61	TCCTGCAAGGGTGTGGCTACACATTCACCTGATATGCTATGACATGGGGTGAAGCAGAGT	120
Qy	121	CATGAAAGAGCCTTGAGTGTATGGAGTATTAATTCCTAACAAATGGTGTACTAACTAC	180
Db	121	CATGAAAGAGCTTAGAGTGTAGAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	180
Qy	181	AAGCAGAGTTCAAGGGCAGGCGCACTTGACTGTAGACAACTGCTCCAGCAGGCTTAC	240
Db	181	AACCAAGATTTCAGGGCGAAGGCCCAATGACTGTAGACAAATCTCCAGCAGGCTTAT	240
Qy	241	ATGAGACTCCGCAAGCCTGACATCTTGAGAGATTCGTGAGTCTATTAATTAATTAATTAAT	297
Db	241	ATGAGAACTTGGCAGACTGACATCTGAGAGATTCGTGAGTCTATTAATTAATTAATTAATTAAT	300
Qy	298	ACTACGGTCCCGTTTGTCTTAATCTGGGTTCCAAAGGACCAAGGTCACCGTCTCTCAAGTGA	357
Db	301	ACTATGTCTCTTACTTGACTACTGGGGCCAAAGTGAACACGGTCAACCGTCTCTCAAGTGA	360
Qy	358	GGCGGTTCAAGGGGAGGAGTGGGCTCTGGCGGTTGGCGGATCGGACATGAGGCTCATAGTCT	417
Db	361	GGCGGTTCAAGGGGAGGAGTGGGCTCTGGCGGTTGGCGGATCGGACATGAGGCTCATAGTCT	420
Qy	418	CCAGCAATCATGTCTGCATCTTCCAGAGGGAGAAAGTCAACCATGACCTGCAGTGGCAGCTCA	477
Db	421	CCAGCAATCATGTCTGCATCTTCCAGAGGGAGAAAGTCAACCATGACCTGCAGTGGCAGCTCA	480
Qy	478	AGTATTAAGTTACATGCACTGGTACCAAGCAAGAGCCTGTACCTCCGCCAAAGATGGATT	537
Db	481	AGTATTAAGTTACATGCACTGGTATAGCAAGAAAGCAGGCACTCCGCCAAAGATGGATT	540
Qy	538	TATGACATATCCAAACTGGGCTTCTGAGAGTCCCTGCTGCTTCAAGTGGCAGTGGGATCTGGG	597
Db	541	TATGACATATCCAAACTGGGCTTCTGAGAGTCCCTGCTGCTTCAAGTGGCAGTGGGATCTGGG	600
Qy	598	ACCTCTTATTTCTCTCAATCAGCAGCATGAGAGCTGTAGATGCTGCCATTATTAATCTGC	657
Db	601	ACCTCTTATTTCTCTCAATCAGCAGCATGAGAGCTGTAGAGATGCTGCCATTATTAATCTGC	660
Qy	658	CATCAGCGAGTAGTTACCCGCTCAGCTTCGGTCTGGGACACAGTTGGAAATTAATA 714	
Db	661	CATCAGCGAGTAGTTACCCCAATTCAGTTCGGAGGGGGGCCAAGCTGGAAATTAATAA 717	
RESULT 5			
AAL51099			
ID	AAL51099 standard; DNA; 717 BP.		
AC	AAL51099;		
DT	27-FEB-2003 (first entry)		
DE	Human neurological/CNS disease treatment method-related gene.		
KW	Gene: ds; vaccine; gene therapy; neurological disease; CNS disorder;		
KW	central nervous system disorder; olfactory system; Alzheimer's disease;		
KW	Creutzfeldt-Jakob disease; Huntington's chorea; Parkinson's disease;		
KW	viral infection of the brain; brain tumour; lysosomal storage disease;		
KW	multiple sclerosis.		
OS	Homo sapiens.		
FN	WO200274243-A2.		
PD	26-SEP-2002.		
PF	15-MAR-2002; 2002MO-US008042.		
XX	PR 15-MAR-2001; 2001US-00808037.		
XX			

PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
 PA (MCIN/) MCINNIS P.
 XX Solomon B, Frenkel D;
 XX WPI; 2003-040542/03.
 DR P-PSDB; AA016066.
 XX
 PT Treating or diagnosing neurological diseases of the central nervous
 PT system, e.g. Alzheimer's disease, comprises displaying a polypeptide or
 PT diagnostic agent on viral display vehicle and introducing or detecting
 PT the display vehicle.
 XX
 PS Example 2; Fig 11A; 214pp; English.
 XX
 CC The invention comprises a method for treating a neurological disease or a
 CC central nervous system (CNS) disorder. The method involves displaying a
 CC therapeutic molecule capable of treating the neurological disease or CNS
 CC disorder on a viral display vehicle. The viral display vehicle is then
 CC introduced into the olfactory system of a subject to treat the disease or
 CC disorder. The method of the invention is useful for preventing, treating
 CC and diagnosing neurological diseases or CNS disorders, such as:
 CC Alzheimer's disease; Creutzfeldt-Jakob disease; Huntington's chorea; viral
 CC infections of the brain; brain tumours; lysosomal storage diseases;
 CC Parkinson's disease; and multiple sclerosis. The present DNA sequence
 CC represents a gene which was used in the invention
 XX
 SQ Sequence 717 BP; 178 A; 174 C; 198 G; 167 T; 0 U; 0 Other;
 Query Match 82.8%; Score 593.4; DB 10; Length 717;
 Best Local Similarity 90.1%; Pred. No. 4e-158;
 Matches 646; Conservative 0; Mismatches 68; Indels 3; Gaps 1;
 Oy 1 CAGGTGAAACTGCGACGATCGACCTGAGTGTGAGGCTGGGCTTCAGTGAATTA 60
 Db 1 CAGGTGAAACTGCGACGATCGAGGCTGAGTGTGAGGCTGGGCTTCAGTGAATTA 60
 Oy 61 TCCTGCAAGACTCTGAGAACAAATTCAGTGAATGACAGCACTGGGTGAAGAGGC 120
 Db 61 TCCTGCAAGAGGTTCTGGCTACACATTCAGTGAATGACAGCACTGGGTGAAGAGGC 120
 Oy 121 CATGAAAGAGCTTGTAGTGTGAGTGAATTAATCTTAACATGATGTGTAATCACTAC 180
 Db 121 CATGAAAGAGCTTGTAGTGTGAGTGAATTAATCTTAACATGATGTGTAATCACTAC 180
 Oy 181 AAGCAAGAGTTCAGAGGCGCAAGCCATGATGTAAGCAAGTCTCCAGACAGCCTAC 240
 Db 181 AAGCAAGAGTTCAGAGGCGCAAGCCATGATGTAAGCAAGTCTCCAGACAGCCTAT 240
 Oy 241 ATGAGAGCTCCGAGCTGACATCTGAGAGTCTGAGTCTTATCTGCAAGGAGGCT 297
 Db 241 ATGAGAGCTCCGAGCTGACATCTGAGAGTCTGAGTCTTATCTGCAAGGAGGCT 300
 Oy 298 ACTACGGTCCCGTTGCTTACTTGAGTCCAGAGGACCAAGGTCACCGTCTCTCAGTGA 357
 Db 301 ACTATGTCCTACTTTGACTTACCTGGGCGCAAGTGAACAGGTCACCGTCTCTCAGTGA 360
 Oy 358 GGGCGTTGAGGCGGAGTGTGCTTGGCGGTGGCGAGTGAACATGAGCTCACTAGTCT 417
 Db 361 GGGCGTTGAGGCGGAGTGTGCTTGGCGGTGGCGAGTGAACATGAGCTCACTAGTCT 420
 Oy 418 CCAGCATCATGTCTGATCTCCAGGGGAGAAAGTCAACATGAGTGAAGTGAAGTCA 477
 Db 421 CCAGCATCATGTCTGATCTCCAGGGGAGAAAGTCAACATGAGTGAAGTGAAGTCA 480
 Oy 478 AGTATAGTTCATGACACTGTGTACAGAGAAAGCTGTCACTCCCAAAAGATGAT 537
 Db 481 AGTATAGTTCATGACACTGTGTGTACAGAGAAAGCTGTCACTCCCAAAAGATGAT 540
 Oy 538 TATGACATCATCAAACTGGCTTCTGAGTCCCTGCTGCTTCACTGAGTGGAGTCTGG 597
 Db 541 TATGACATCATCAAACTGGCTTCTGAGTCCCTGCTGCTTCACTGAGTGGAGTCTGG 600

Oy 598 ACCTCTTATCTCTACATGACAGATGAGGCTGTAGATGCTGACCACTTAATTAATGTC 657
 Db 601 ACCTCTTATCTCTACATGACAGATGAGGCTGTAGATGCTGACCACTTAATTAATGTC 660
 Oy 658 CATGAGCGAGTGAATTAACCGCTCAAGTTCGCTGTGGAGACAGTTGAAATTA 714
 Db 661 CATGAGCGAGTGAATTAACCGCTCAAGTTCGCTGTGGAGAGCGGCGCAAGTGAATTA 717
 XX
 PS RESULT 6
 ADJ88112
 ID ADJ88112 standard; DNA; 717 BP.
 XX
 AC ADJ88112;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human beta amyloid peptide antibody (508) heavy chain DNA.
 XX
 KW Neurological disease; central nervous system; CNS disorder;
 KW plaque-forming disease; Alzheimer's disease; SAA amyloidosis;
 KW hereditary Icelandic syndrome; senility; multiple myeloma; scrapie;
 KW bovine spongiform encephalopathy; BSE; kuru; Creutzfeldt-Jakob disease;
 KW CJD; Gerstmann-Strausler-Sheinker disease; GSS; fatal familial insomnia;
 KW FFI; non-plaque-forming disease; Huntington's chorea; viral infection;
 KW brain tumour; lysosomal storage disease; neurodegeneration;
 KW multiple sclerosis; vaccine; beta amyloid peptide; beta AP; antibody;
 KW human; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Location/Qualifiers
 FT 1..717
 FT /*tag= a
 FT /product= "508 antibody heavy chain protein"
 FT /partial
 FT /note= "No start and stop codon"
 XX
 PN US2004013647-A1.
 XX
 PD 22-JAN-2004.
 XX
 PF 11-MAR-2003; 2003US-00384788.
 XX
 PR 03-SEP-1999; 99US-0152417P.
 PR 29-DEC-1999; 99US-00473653.
 PR 31-JUL-2000; 2000US-00629971.
 PR 31-AUG-2000; 2000WO-11000518.
 PR 15-MAR-2001; 2001US-00808037.
 PR 07-AUG-2001; 2001US-00830954.
 PR 12-APR-2002; 2002US-03171735P.
 PR 06-JUN-2002; 2002US-00162889.
 XX
 PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
 XX
 PI Solomon B, Frenkel D;
 XX WPI; 2004-108188/11.
 DR P-PSDB; ADJ88113.
 XX
 PT Treating neurological disease CNS e.g., Alzheimer's disease, by
 PT displaying therapeutic molecule capable of treating the disease on viral
 PT display vehicle which is then administered to subject through olfactory
 PT system.
 XX
 PS Example 2; SEQ ID NO 5; 68pp; English.
 XX
 CC The invention relates to a method of treating a neurological disease or
 CC disorder of the central nervous system (CNS). The method involves
 CC displaying a therapeutic molecule capable of treating the neurological
 CC disease or disorder of the CNS on a viral display vehicle and introducing
 CC viral display vehicle into a subject by applying an effective amount of
 CC the viral display vehicle displaying the therapeutic molecule to an

CC olfactory system of the subject. The method is useful for treating a
CC neurological disease or disorder of CNS such as a plaque-forming disease
CC such as Alzheimer's disease, late onset Alzheimer's disease,
CC presymptomatic Alzheimer's disease, SMA amyloidosis, hereditary Icelandic
CC syndrome, senility, multiple myeloma, scrapie, bovine spongiform
CC encephalopathy (BSE), kuru, Creutzfeldt-Jakob disease (CJD), Geistmann-
CC Streussler-Scheinker disease (GSS) or fatal familial insomnia (FFI). The
CC method is also useful for treating a non plaque forming disease or
CC disorder e.g. Huntington's chorea, viral infections of the brain, brain
CC tumours, lysosomal storage diseases which cause neurodegeneration and are
CC manifested by enzyme deficiencies and multiple sclerosis. The invention
CC is also used in the preparation of vaccines. The present sequence is
CC human beta amyloid peptide (beta AP) antibody heavy chain DNA. This
CC sequence is used to illustrate the method of the invention.

SQ Sequence 717 BP; 178 A; 174 C; 198 G; 167 T; 0 U; 0 Other;

Query Match 82.8%; Score 593.4; DB 12; Length 717;

Matches 646; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

QY	1	CAGGTAAACTGCAGAGCTCAGACCTGTAACCTGTGGGAGCTTCAGTAAAGTA	60
Db	1	CAGGTCAACTGCAGAGCTCAGGGGCTGAGCTGTGAGGCTTGAGTAAGATT	60
QY	61	TCTCTGAAGACTTCTTGAGAACAAATTCACTGAATACACCATGACCTGGGTGAACAGAGC	120
Db	61	TCTCTGAAGAGGTTCTGGCTACACATTCACTGATTTATGTCTATGACTGGGTGAACAGAGT	120
QY	121	CATGGAAGAGCGCTTCAATGTGAATTTGAGAGTATTAATCTTAACATGTGGTGAATTAATAC	180
Db	121	CATGCAAGAGCTTAAGTGTGAATTTGAGAGTATTAATTAATTAATTAATGATGATGCTAC	180
QY	181	AACCAAGAGTTCAGGGCAAGGCCAACATGACTGTGACCAATCCTCCAGCAGCGCTAT	240
Db	181	AACCAAGAGTTCAGGGCAAGGCCAACATGACTGTGACCAATCCTCCAGCAGCGCTAT	240
QY	241	ATGAGAGCTCCGAGCGCTGACATCTAGATTTCTGAGATCTTATCTACTGTGCAAG--GAT	297
Db	241	ATGGAACCTTGCAAGACTGACATCTAGAGTTCTGACATCTTATCTGTGCAAGGGGCT	300
QY	298	ACTACGCTCCCGTTTGGCTTACTGAGGTCCAAAGGACCAAGCTCACCGTCTCTCAGGTGA	357
Db	301	ACTATGCTCTACTTTGACTACTGAGGCAAGTGAACAAGTCAACGTTCTCTCAGGTGA	360
QY	358	GGGGGTTCAAGCGAGGTGGCTTCTGGCGGTGGCGATGTGAACATGAGCTCACTCACTT	417
Db	361	GGGGGTTCAAGCGGAAATGTGGCTTCTGGCGGTGGCGATGTGACATGAGCTCACTCACTT	420
QY	418	CCAGCAATCATGTCTGCACTCTCCAGGGGAGAAAGTCAACATGACCTGCAAGTGGCAGCTCA	477
Db	421	CCAGCAATCATGTCTGCACTCTCCAGGGGAGAAAGTCAACATGACCTGCAAGTGGCAGCTCA	480
QY	478	AGTATAAGTTACATGCACTGTTACAGCAGAAAGCGTCACTCTCCCAAAAGATGATT	537
Db	481	AGTATAAGTTACATGCACTGTTATCAGCAGAAAGCGACCTCCCAAAAGATGATT	540
QY	538	TATGACATATCCAAACTGGCTCTGGAAGTCCGTGCTCAATGCAAGTGGGTCTGGG	597
Db	541	TATGACATATCCAAACTGGCTCTTGAAGTCCGTGCTCAATGCAAGTGGGTCTGGG	600
QY	598	ACCTCTTATTTCTCAATCAGCAGCATGAGGCTGTAGATGTGCACTTATTAATTCG	657
Db	601	ACCTCTTATTTCTCAATCAGCAGCATGAGGCTGTAGATGTGCACTTATTAATTCG	660
QY	658	CATCAGCGAGTAAATTAATCCCGCTCACGTTCCGTCTGGGACACACTTGGAAATATAA	714
Db	661	CATCAGCGGAGTAAATTAATCCCATTAACGTTCCGAGGGGGGGCAAGCTGTGAAATATAA	717

XX	AC	ACC83315;
XX	DT	29-AUG-2003 (first entry)
XX	DE	Single chain antibody encoding DNA #SEQ ID 19

KM Tumor; drug delivery; ligand; cancer; carcinoma; bladder; breast;
 KM cervix; colorectum; lung; ovary; pancreas; prostate; stomach;
 cholangiocarcinoma; gastric sarcoma; glioma; lymphoma; melanoma;
 KM multiple myeloma; osteosarcoma; head; neck; radiation; x-ray; gene
 antibody; ds

OS Synthetic.

FH	Key	Location/Qualifiers
FT	CDS	1. .726

PN WO2003028640-A2.

PD 10-APR-2003

PF 27-SEP-2002; 2002WO-US030917.

PR 03-OCT-2001; 2001US-0328123P.

PA (UYVA-) UNIV VANDERBILT.

PI Hallahan DE, Qu S;
yy

DR WPI; 2003-421186/39.

PT Identifying molecule that binds to irradiated tumor in a subject, by PT exposing tumor to ionizing radiation, administering library of diverse PT molecules and isolating library molecules from tumor to identify the PT target.

PS Claim 38; Page 106-107; 108pp; English.

CC The invention relates to a method for identifying a molecule that binds
CC an irradiated tumour in a subject. The method of the invention involves
CC exposing a tumour to ionizing radiation, administering a library of
CC diverse molecules to a subject, and isolating one or more molecules of
CC the library from the tumour. The method of the invention is useful for
CC identifying a molecule that binds an irradiated tumour in a subject e.g.
CC warm-blooded vertebrate and human, and also for tumour detection. The
CC tumour is a primary or a metastasized tumour such as carcinoma of the
CC bladder, breast, cervix, colorectum, lung, ovary, pancreas, prostate,
CC stomach, cholangiocarcinoma, gastric sarcoma, glioma, lymphoma, melanoma,
CC multiple myeloma, osteosarcoma, head and neck tumor and solid tumor. The
CC method of the invention is useful for X-ray-guided delivery of a
CC therapeutic composition, a diagnostic composition or their combinations
CC to a tumour in a subject. The current sequence represents a single chain
CC antibody encoding sequence that was identified following *in vivo* panning
CC to irradiated tumours. This antibody binds platelet membrane glycoprotein
CC IIb

SQ Sequence 726 BP; 177 A; 183 C; 201 G; 165 T; 0 U; 0 Other;

Query match	80.1%;	Score 574;	DB 8;	Length 726;
-------------	--------	------------	-------	-------------

Matches 635; Conservative 0; Mismatches 82; Indels 3; Gaps 1;

Qy 1 CAGGTGAACTGCAGCAGTCAGGACCTGAACTGGTGNAGCCTGGGGCTTCAGTGAAGATA 60
|||||
7 CAGGTCAACCTGCAGCAGTCAGGACCTGAGTGGTAAAGCCTGGGGCTTCAGTGAAGATA 66
Db

Qy 61 TCTCGAAGACTTCTGSAACAAATTCTGATACACCATGACCTGGGTGAGCAGAGC 120
Nb 67 TCTCGAAGGCTTCTGATACACATTCTAGCTATGTATGACTGGGTGAGCAGAGC 126

QY 121 CATGAAAGAGCTTGGAGTATGAGTATTAATCTTAACATATGTTGTTACTACTAC 180
DB 127 CTTGGGAGGAGCTTGGAGTATGAGTATTAATCTTAACATATGTTGTTACTACTAC 186
QY 181 AAGCAGAAGTTCAGAGGAGGAGCCATTTGATCTGATGACCAAGTCTCCAGACAGCTTAC 240
DB 187 AATGAGAGTTTCAAGGAGGAGCCGACCTGATCTGATGACCAAGTCTCCAGACAGCTTAC 246
QY 241 ATGAGCTCCGAGCTTGAATCTGAGATTTCTGATGATCTTATCTGATGACCAAGTCT 297
DB 247 ATGAGCTCCGAGCTTGAATCTGAGATTTCTGATGATCTTATCTGATGACCAAGTCT 306
QY 298 ACTACGCTCCGAGCTTGAATCTGAGATTTCTGATGATCTTATCTGATGACCAAGTCT 357
DB 307 AACTACGCTCCGAGCTTGAATCTGAGATTTCTGATGATCTTATCTGATGACCAAGTCT 366
QY 358 GCGGTTTCAAGGAGGAGTGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
DB 367 GCGGTTTCAAGGAGGAGTGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 426
QY 418 CCAGCATATGTTGATCTTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 477
DB 427 CCAACATATGTTGATCTTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 486
QY 478 AGTAAATGTTATGATCTTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 537
DB 487 AGTAAATGTTATGATCTTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 546
QY 538 TATGACATATGTTGATCTTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 597
DB 547 TATGACATATGTTGATCTTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 606
QY 598 ACCCTTATTTCTTCAATCATGACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 657
DB 607 ACCCTTATTTCTTCAATCATGACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 666
QY 658 CATGAGGAGGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 717
DB 667 CATGAGGAGGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 726

RESULT 8
ADT91208
ID ADT91208 standard; DNA; 726 BP.

ADT91208;
16-DEC-2004 (first entry)

DE Single chain variable fragment (scfv) antibody encoding DNA #2.
DB
XX Tumour; benign intracranial meningioma; arteriovenous malformation;
XX angiolipoma; macular degeneration; melanoma; adenocarcinoma;
XX malignant glioma; prostatic carcinoma; kidney carcinoma;
XX bladder carcinoma; pancreatic carcinoma; thyroid carcinoma;
XX lung carcinoma; colon carcinoma; rectal carcinoma; brain carcinoma;
XX liver carcinoma; breast carcinoma; ovarian carcinoma; angiolipoma;
XX retrofetal fibroplasia; haemangioma; Kaposi's sarcoma;
XX single chain variable fragment; scfv; gene; ds.

OS unidentified.

XX Location/Qualifiers
FH Key 1.726
FT CDS

FT /*tag= a
FT /product= "Single chain variable fragment (scfv)
FT /antibody=" antibody"
FT /partial
FT /note= "No stop codon"

XX US2004191249-A1.

PD 30-SEP-2004.
XX
XX 20-OCT-2003; 2003US-00689006.
XX
XX 28-APR-2000; 2000WO-US011485.
PR 09-NOV-2001; 2001US-00914605.
PR 27-SEP-2002; 2002US-00259087.
XX
XX (UVA-) UNIV VANDERBILT.
XX
XX Hallahan DE, Mernaugh R;
PI WPI; 2004-698661/68.
DR P-PSDB; ADT91209.
XX
XX Screening phage-displayed antibodies binding to radiation-inducible
PT neointigen on cell, comprises contacting cell with antibodies, treating
PT cell with radiation, contacting cell with antibodies not binding to cell,
PT detecting bound antibody.
XX
XX Claim 4; SEQ ID NO 19; 64bp; English.

CC The invention relates to a method for screening phage-displayed
CC antibodies binding to radiation-inducible neointigen on cell. The method
CC involves contacting cell with antibodies, treating cell with radiation,
CC contacting cell with antibodies not binding to cell and detecting the
CC bound antibody. The method is useful for screening several phage-
CC displayed antibodies for an ability to bind to a radiation-inducible
CC neointigen present on a cell, where the cell is tumour cell chosen from
CC benign intracranial meningiomas, arteriovenous malformation, angiolipoma,
CC macular degeneration, melanoma, adenocarcinoma, malignant glioma,
CC prostatic carcinoma, kidney carcinoma, bladder carcinoma, pancreatic
CC carcinoma, thyroid carcinoma, lung carcinoma, colon carcinoma, rectal
CC carcinoma, brain carcinoma, liver carcinoma, breast carcinoma, ovary
CC carcinoma, solid tumours, solid tumour metastases, angiolipomas,
CC retrofetal fibroplasia, haemangiomas, Kaposi's sarcoma, head and neck
CC carcinomas and their combinations or vascular endothelial cell. The
CC present sequence is a DNA encoding single chain variable fragment (scfv)
CC antibody that binds to radiation-inducible neointigens.
XX
XX Sequence 726 BP; 177 A; 183 C; 201 G; 165 T; 0 U; 0 Other;

Query Match 80.1%; Score 574; DB 13; Length 726;
Best Local Similarity 88.2%; Pred. No. 1.3e-153;
Matches 635; Conservative 0; Mismatches 82; Indels 3; Gaps 1;

QY 1 CAGGTGAAGTTCAGAGCTGAGACCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
DB 7 CAGGTGAAGTTCAGAGCTGAGACCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 66
QY 61 TCCGCAAGAGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
DB 67 TCCGCAAGAGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 126
QY 121 CATGAAAGAGCTTGAAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
DB 127 CTTGGGAGGAGCTTGAAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 186
QY 181 AAGCAGAAGTTCAGAGGAGGAGCCATTTGATCTGATGACCAAGTCTCCAGACAGCTTAC 240
DB 187 AATGAGAGTTTCAAGGAGGAGCCGACCTGATCTGATGACCAAGTCTCCAGACAGCTTAC 246
QY 241 ATGAGCTCCGAGCTTGAATCTGAGATTTCTGATGATCTTATCTGATGACCAAGTCT 297
DB 247 ATGAGCTCCGAGCTTGAATCTGAGATTTCTGATGATCTTATCTGATGACCAAGTCT 306
QY 298 ACTACGCTCCGAGCTTGAATCTGAGATTTCTGATGATCTTATCTGATGACCAAGTCT 357
DB 307 AACTACGCTCCGAGCTTGAATCTGAGATTTCTGATGATCTTATCTGATGACCAAGTCT 366
QY 358 GCGGTTTCAAGGAGGAGTGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
DB 367 GCGGTTTCAAGGAGGAGTGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 426

QY 662 AGCGAGTATTACCCGCTCACGTTCCGTCGGGACACAGTTGGAAATTAACCG 717
DB 800 AGCGAGTATTACCCGCTCACGTTCCGTCGGGACACAGTTGGAAATTAACCG 855

RESULT 10
ID ADT91212 standard; DNA; 786 BP.
AC ADT91212;
DT 16-DEC-2004 (first entry)
DE Single chain variable fragment (scfv) antibody encoding DNA #4.
KM Tumour; benign intracranial meningioma; arteriovenous malformation;
KM anglioma; macular degeneration; melanoma; adenocarcinoma;
KM malignant glioma; prostatic carcinoma; kidney carcinoma;
KM bladder carcinoma; pancreatic carcinoma; thyroid carcinoma;
KM lung carcinoma; colon carcinoma; rectal carcinoma; brain carcinoma;
KM liver carcinoma; breast carcinoma; ovary carcinoma; angiofibroma;
KM retroental fibroplasia; haemangioma; Kaposi's sarcoma;
KM single chain variable fragment; scfv; gene; ds.
OS Unidentified.
FH Key Location/Qualifiers
FT 1..786
FT /*tag= a
FT /product= "Single chain variable fragment (scfv)
FT antibody"

US2004191249-A1.
XX 30-SEP-2004.
PD 20-OCT-2003; 2003US-00689006.
XX 28-APR-2000; 2000WO-US011485.
PR 09-NOV-2001; 2001US-00914605.
PR 27-SEP-2002; 2002US-00259087.
XX (UYVA-) UNIV VANDERBILT.
PA Hallahan DE, Mernaugh R;
PI P-PSDB; ADT91213.
DR WPI; 2004-698661/68.
DR P-PSDB; ADT91213.
XX
PT Screening phage-displayed antibodies binding to radiation-inducible
PT neantigen on cell, comprises contacting cell with antibodies, treating
PT cell with radiation, contacting cell with antibodies not binding to cell,
PT detecting bound antibody.
XX
PS Claim 4; SEQ ID NO 23; 64pp; English.
XX The invention relates to a method for screening phage-displayed
CC antibodies binding to radiation-inducible neantigen on cell. The method
CC involves contacting cell with antibodies, treating cell with radiation,
CC contacting cell with antibodies not binding to cell and detecting the
CC bound antibody. The method is useful for screening several phage-
CC displayed antibodies for an ability to bind to a radiation-inducible
CC neantigen present on a cell, where the cell is tumour cell chosen from
CC benign intracranial meningiomas, arteriovenous malformation, anglioma,
CC macular degeneration, melanoma, adenocarcinoma, malignant glioma,
CC prostatic carcinoma, kidney carcinoma, bladder carcinoma, pancreatic
CC carcinoma, thyroid carcinoma, lung carcinoma, colon carcinoma, rectal
CC carcinoma, brain carcinoma, liver carcinoma, breast carcinoma, ovary
CC carcinoma, solid tumour metastases, angiofibromas,
CC retroental fibroplasia, haemangiomas, Kaposi's sarcoma, head and neck
CC carcinomas and their combinations or vascular endothelial cell. The
CC present sequence is a DNA encoding single chain variable fragment (scfv)
CC antibody that binds to radiation-inducible neantigen.

XX SQ Sequence 786 BP; 185 A; 200 C; 224 G; 177 T; 0 U; 0 Other;
Query Match 78.3%; Score 561.4; DB 13; Length 786;
Best Local Similarity 87.0%; Pred. No. 5.1e-149;
Matches 629; Conservative 0; Mismatches 88; Indels 6; Gaps 1;

QY 1 CAGGTGAACCTGACGAGCTGAGCACTGAACTGGTGNAGCCTGGGGCTTCAGTAAAGTA 60
DB 7 CAGGTGAACCTGACGAGCTGAGCACTGAGCTGGTAAAGCCTGGGGCTTCAGTAAAGT 66
QY 61 TCCTGCAAGACTTGTGANNCAATTCATGAAATACACATGCACTGGGTGAAGCAGC 120
DB 67 TCCTGCAAGACTTGTGANNCAATTCATGAAATACACATGCACTGGGTGAAGCAGC 126
QY 121 CATGGAAGAGCCTTGAAGTGAATGAGATTTAATCTTAACAATGGTGTACTAATAC 180
DB 127 AATGGAAGAGCCTTGAAGTGAATGAGATTTAATCTTAACAATGGTGTACTAATAC 186
QY 181 AAGGAGAAGTTCAGAGGCAAGGCAATTCAGTGTAGCAAGTCTCAGACAGCCTAC 240
DB 187 AAGGAGAAGTTCAGAGGCAAGGCAATTCAGTGTAGCAAGTCTCAGACAGCCTAC 246
QY 241 ATGAGACTCCGACGCTGACATCTGAGGATTCGAGTATTAATCTGTGCAAGA----- 294
DB 247 ATGAGACTCCGACGCTGACATCTGAGGATTCGAGTATTAATCTGTGCAAGA----- 306
QY 295 GATACCTACGCTCCGTTGCTTACTGAGTCCAGAGGACACGCTGACCTCTCTCAGCT 354
DB 307 GATACCTACGCTCCGTTGCTTACTGAGTCCAGAGGACACGCTGACCTCTCTCAGCT 366
QY 355 GGAGGCGGTTCCAGGCGAGAGGCTGCTGCGGCGGTGGCGGATGGACATGAGCTCACTAG 414
DB 367 GGAGGCGGTTCCAGGCGAGAGGCTGCTGCGGCGGTGGCGGATGGACATGAGCTCACTAG 426
QY 415 TCTCAGCAATCATGCTGTCATCTCCAGGAGAGGATCAACATGACCTGCGAGTGCAGC 474
DB 427 TCTCAGCAATCATGCTGTCATCTCCAGGAGAGGATCAACATGACCTGCGAGTGCAGC 486
QY 475 TCAAGTATAGTATCATGCACTGTTACAGCAGAGCCTGTCACTCCCAAAAGATGG 534
DB 487 TCAAGTATAGTATCATGCACTGTTACAGCAGAGCCTGTCACTCCCAAAAGATGG 546
QY 535 ATTATGACATCATGCACTGTTACAGCAGAGCCTGTCACTCCCAAAAGATGG 594
DB 547 ATTATGACATCATGCACTGTTACAGCAGAGCCTGTCACTCCCAAAAGATGG 606
QY 595 GGAGCTCTTATTTCTCAACATGAGCAGATGAGGCTGTAGATGTGCACTTATTAC 654
DB 607 GGAGCTCTTATTTCTCAACATGAGCAGATGAGGCTGTAGATGTGCACTTATTAC 666
QY 655 TGCCATCAGCGAGTATTACCGGCTCAGCTGGTGTGAGACACAGTTGAAATTA 714
DB 667 TGCCATCAGCGAGTATTACCGGCTCAGCTGGTGTGAGACACAGTTGAAATTA 726
QY 715 CGG 717
DB 727 CGG 729

RESULT 11
ID ADCT9233 standard; DNA; 716 BP.
AC ADCT9233;
DT 01-JAN-2004 (first entry)
DE VK-8-1.9 scfv nucleotide sequence SEQ ID NO:1.
XX CA 125 tumour antigen; CA 125 tumour antigen modulator;
KW CA 125 tumour antigen-associated disease; cytostatic; gene therapy; gene;
KW ds.

XX	Synthetic.
OS	WO2003076465-A2.
XX	
PN	18-SEP-2003.
XX	
PD	11-MAR-2003; 2003WO-CA000341.
XX	
PF	11-MAR-2002; 2002US-0363306P.
XX	
PR	28-FEB-2003; 2003CA-02420494.
XX	
XX	(UYSH) UNIV SHERBROOKE.
PA	
XX	
FI	Rancourt C, Piche A, Beaudin J;
DR	WPI, 2003-722323/68.
XX	
PT	New modulator capable of negatively modulating a CA 125 tumor antigen in
XX	a mammalian cell, useful for preparing a composition for preventing or
PT	treating CA 125 tumor antigen-associated disease in a mammal.
XX	
PS	Claim 7; SEQ ID NO 1; 90pp; English.
XX	
CC	The present invention describes a modulator capable of negatively
CC	modulating a CA 125 tumour antigen in a mammalian cell. Also described:
CC	(1) a recombinant nucleic acid comprising at least one sequence selected
CC	from the group consisting of ADC79233, ADC79234, ADC79235, ADC79236,
CC	ADC79237 and ADC79238; (2) a vector comprising the recombinant nucleic
CC	acid; (3) a host cell; (4) a pharmaceutical composition; (5) preventing
CC	or treating CA 125 tumour antigen-associated disease in a mammal; and (6)
CC	negatively modulating a CA 125 tumour antigen in a mammalian cell. A
CC	modulator capable of negatively modulating a CA 125 tumour antigen has
CC	cytostatic activity, and can be used in gene therapy. The modulator,
CC	recombinant nucleic acid, vector or host cell can be used for preparing a
CC	composition for preventing or treating CA 125 tumour antigen-associated
CC	disease in a mammal.
XX	
SQ	Sequence 716 BP; 170 A; 191 C; 196 G; 159 T; 0 U; 0 Other;
XX	
Query Match	77.5%; Score 555.8; DB 10; Length 716;
Best Local Similarity	87.7%; Pred. No. 1.9e-147;
Matches 629; Conservative	0; Mismatches 84; Indels 4; Gaps 2.
QY	1 CAGGTGAAATCTGCAGACAGTCAAGACCTGAACCTGTGAGGCTTGAGTGAAGATA 60
DB	1 CAGGTCCAGCTCAGAGAGTCAAGACCTGAACCTGTGAGGACCTTGAGTGAAGATA 60
QY	61 TCTCTGCAAGACTTCTGAGNACCAATTCTACTGAATACACCATGCACTGGGTGAAGAGCC 120
DB	61 TCTCTCAAG-CTTCTGGAATACCAATTCTACTGAATACACCATGCACTGGGTGAAGAGCC 119
QY	121 CATGAAAGAGCCTTGAGTGAAGTGGAGTATTAATCCTAACAATGAGTGTACTAATC 180
DB	120 CATGAAAGAGCCTTGAGTGAAGTGGAGTATTAATCCTAACAATGAGTGTACTAATC 179
QY	181 AAGCAGAAATTCAAGGGCAGAGCCCAATTGACTGTAGACAAGTCTCTCAGCAGACCTTAC 240
DB	180 AACGAGAATTCAAGGAAAGAGCCCTCTTGAAGTGAACACTCTCCAGCAGACACTTAC 239
QY	241 ATGAGAGCTCCGAGCCTGACATCTGAGGATTTTGCAGTCTATTACTGTGCAAGAGATCT 300
DB	240 ATGAGAGCTCCGAGCCTGACATCTGAGGATTTTGCAGTCTATTACTGTGCAAGAGATCT 299
QY	301 ACGGACCCG---TTTGCTTACTAGGGTCCAAAGGACCAAGGTCAACGCTCCCTCAGGTGA 357
DB	300 GGGTTTGGTACTTGATGATCTCTGGGACCAAGGACCAAGGTCAACGCTCTCTCAGGTGA 359
QY	358 GGGCGTTACGGCGAGAGTGGCTCTGGCGGTGGCGATCGACATCGAGCTCACTAGTCT 417
DB	360 GGGCGTTACGGCGAGAGTGGCTCTGGCGGTGGCGATCGACATCGAATGACCAAGTCT 419
QY	418 CCAGCAATCATCTTCATCTCCAGGGGAGAAAGTCAACCATGACCTGCAGTGGCAGCTCA 477

Db	420	CCAGGAAATTCGTCTGTCATCTTCACAGGGAGAAAGTCAATATGACTTGCAGGGCCACCCCA	479
Qy	478	AGTATAGTTACATGCACTGATGATACAGCAGAAAGCCTGTCACTCCCAAAAGATGATT	537
Db	480	AGTATAGTTACATGCACTGATGATACAGCAGAAAGCAGATATCTCCCCAAACCTTGATT	539
Qy	538	TATGACACATCCAAATGCGCTTCTGGAATCCCTGCTCGCTTACATAGTGGCAGTGGGTCTGG	597
Db	540	TATACCAATCCAACTGGCTTCTGGAATCCCTGCTCGCTTACATAGTGGCAGTGGGTCTGG	599
Qy	598	ACCTCTTATCTCTCACAATGACATGACAGATGAGGCTGTATGATGCTGCCACTTATTAATGTC	657
Db	600	ACCTCTTATCTCTCTCAATGACATGACAGATGAGGCTGTATGATGCTGCCACTTATTAATGTC	659
Qy	658	CATCAGCGAGTATGTTACCCCGCTCAGTTCGGTGTCTGGGACACAGTTGGAAATATAA	714
Db	660	CAGCAGTGGAGTGTATGAGCCACCAACGTTCCGTTGTGGCACCMAAGCTGGAAATATAA	716
RESULT 12			
ID	ACC83314	standard; DNA; 726 BP.	
XX	ACC83314;		
XX	29-AUG-2003	(first entry)	
DE	Single chain antibody encoding DNA #SEQ ID 17.		
XX			
KW	Tumour; drug delivery; ligand; cancer; carcinoma; bladder; breast;		
KW	cervix; colorectum; lung; ovary; pancreas; prostate; stomach;		
KW	choleangiocarcinoma; gastric sarcoma; glioma; lymphoma; melanoma;		
KW	multiple myeloma; osteosarcoma; head; neck; radiation; x-ray; gene;		
XX	antibody; ds.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..726	
FT		/*tag= a	
FT		/partial	
FT		/note="no stop codon"	
XX			
PN	WO2003028640-A2.		
XX			
PD	10-APR-2003.		
XX			
PF	27-SEP-2002; 2002WO-US030917.		
XX			
PR	03-OCT-2001; 2001US-0328123P.		
XX			
PA	(UYVA-) UNIV VANDERBILT.		
XX			
PI	Hallahan DE, Qu S;		
XX			
DR	WPI; 2003-421186/39.		
PT	P-PsDB; ABR62131.		
XX			
XX			
PS	Claim 38; Page 104-105; 108pp; English.		
CC	The invention relates to a method for identifying a molecule that binds		
CC	an irradiated tumour in a subject. The method of the invention involves		
CC	exposing a tumour to ionizing radiation, administering a library of		
CC	diverse molecules to a subject, and isolating one or more molecules of		
CC	the library from the tumour. The method of the invention is useful for		
CC	identifying a molecule that binds an irradiated tumour in a subject e.g.		
CC	warm-blooded vertebrate and human, and also for tumour detection. The		

CC tumour is a primary or a metastasized tumour such as carcinoma of the
 CC bladder, breast, cervix, colorectum, lung, ovary, pancreas, prostate,
 CC stomach, cholangiocarcinoma, gastric sarcoma, glioma, lymphoma, melanoma,
 CC multiple myeloma, osteosarcoma, head and neck tumor and solid tumor. The
 CC method of the invention is useful for X-ray-guided delivery of a
 CC therapeutic composition, a diagnostic composition or their combinations
 CC to a tumour in a subject. The current sequence represents a single chain
 CC antibody encoding sequence that was identified following in vivo panning
 CC to irradiated tumours. This antibody binds P-selectin

XX Sequence 726 BP; 173 A; 188 C; 202 G; 163 T; 0 U; 0 Other;

Query Match 77.2%; Score 553.2; DB 8; Length 726;

Best Local Similarity 86.4%; Pred. No. 1.1e-146;

Matches 622; Conservative 0; Mismatches 95; Indels 3; Gaps 1;

QY 1 CAGGTGAAACTGACGACGACCTGAACTGCTGAGGCTTCAAGTAAAGATA 60
 DB 7 CAGGTGAAACTGACGACGACCTGAGGCTGAGCTTGATGCTGGGGCTTCAGTGAAGATG 66
 QY 61 TCCGCAAGAGCTTCTGAGAACAAATTCACTGAATACACATGCACTGGGTGAACAGAGC 120
 DB 67 TCTGCAAGGCTTCTGCTGACATCACTGACTGATGATGCTGAGTGAACAGAGG 126
 QY 121 CATGAAAGAGCCTTGAAGTGAAGTGAAGTATTAATCTTAACATGAGTGAATCACTAC 180
 DB 127 CTTGGAAGAGCCTTGAAGTGAAGTGAAGTATTAATCTTGAATGATTAATCACTAC 186
 QY 181 AAGAGAAAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
 DB 187 AATCAAAAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 246
 QY 241 ATGAGAGTCCGACCTGACATCTGAGGATCTGCACTCTTACTGTGC--AAGAGAT 297
 DB 247 ATGAGAGTCCGACCTGACATCTGAGGATCTGCACTCTTACTGTGC--AAGAGAT 306
 QY 298 ACTAGGCTCCGCTTGTCTTACTGAGGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGG 357
 DB 307 TACTATAGCGGATTTGATTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 366
 QY 358 GGGGTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 417
 DB 367 GGGGTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 426
 QY 418 CAGCAATCATGTCTGATCTCCAGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 477
 DB 427 CCAACAAACATGCTGATCTCCAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 486
 QY 478 AGTATAGTTCATGACGCTGGTACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 537
 DB 487 AGTATAGTTCATGACGCTGGTACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 546
 QY 538 TATGACATTCAGAACTGGCTTCTGAGATCCCTGCTGCTTCACTGAGGAGGAGGAGG 597
 DB 547 TATGACATTCAGAACTGGCTTCTGAGATCCCTGCTGCTTCACTGAGGAGGAGGAGG 606
 QY 598 ACCCTTATTTCTTCAACATGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 657
 DB 607 ACCCTTATTTCTTCAACATGAGCTTCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 666
 QY 658 CATCAGGAGGAGTATGACCGCTGACAGGCTGGGTGCTGGGAGACAGAGTTGAAATAAACG 717
 DB 667 CTGCAAGAGAGTATGACCGCTGACAGGCTGGGTGCTGGGAGACAGAGTTGAAATAAACG 726

RESULT 13
 ADT91206
 ID ADT91206 standard; DNA; 726 BP.

XX ADT91206;
 AC
 XX
 DT 16-DEC-2004 (first entry)

DE Single chain variable fragment (scfv) antibody encoding DNA #1.

XX Tumour; benign intracranial meningioma; arteriovenous malformation;
 KM anglioma; macular degeneration; melanoma; adenocarcinoma;
 KM malignant glioma; prostatic carcinoma; kidney carcinoma;
 KM bladder carcinoma; pancreatic carcinoma; thyroid carcinoma;
 KM lung carcinoma; colon carcinoma; rectal carcinoma; brain carcinoma;
 KM liver carcinoma; breast carcinoma; ovary carcinoma; angiofibroma;
 KM retrorenal fibroplasia; haemangioma; Kaposi's sarcoma;
 KM single chain variable fragment; scfv; gene; ds.

OS Unidentified.

XX Location/Qualifiers
 FH Key 1..726
 FT CDS /*tag= a
 FT /product= "single chain variable fragment (scfv)
 FT /antibody"
 FT /partial
 FT /note= "No stop codon"

US2004191249-A1.

30-SEP-2004.

20-OCT-2003; 2003US-00689006.

28-APR-2000; 2000WO-US011485.

09-NOV-2001; 2001US-00914605.

27-SEP-2002; 2002US-00259087.

(UVA-) UNIV VANDERBILT.

XX Hallahan DE, Wernaugh R;

XX WPI; 2004-698661/68.

DR P-PSDB; ADT91207.

PT Screening phage-displayed antibodies binding to radiation-inducible
 PT neantigen on cell, comprises contacting cell with antibodies, treating
 PT cell with radiation, contacting cell with antibodies not binding to cell,
 PT detecting bound antibody.

XX Claim 4; SEQ ID NO 17; 64pp; English.

XX The invention relates to a method for screening phage-displayed
 CC antibodies binding to radiation-inducible neantigen on cell. The method
 CC involves contacting cell with antibodies, treating cell with radiation,
 CC contacting cell with antibodies not binding to cell and detecting the
 CC bound antibody. The method is useful for screening several phage-
 CC displayed antibodies for an ability to bind to a radiation-inducible
 CC neantigen present on a cell, where the cell is tumour cell chosen from
 CC benign intracranial meningiomas, arteriovenous malformation, anglioma,
 CC macular degeneration, melanoma, adenocarcinoma, malignant glioma,
 CC prostatic carcinoma, kidney carcinoma, bladder carcinoma, pancreatic
 CC carcinoma, thyroid carcinoma, lung carcinoma, colon carcinoma, rectal
 CC carcinoma, brain carcinoma, liver carcinoma, breast carcinoma, ovary
 CC carcinoma, solid tumors, solid tumour metastases, angiofibromas,
 CC retrorenal fibroplasia, haemangiomas, Kaposi's sarcoma, head and neck
 CC carcinomas and their combinations or vascular endothelial cell. The
 CC present sequence is a DNA encoding single chain variable fragment (scfv)
 CC antibody that binds to radiation-inducible neantigens.

XX Sequence 726 BP; 173 A; 188 C; 202 G; 163 T; 0 U; 0 Other;

Query Match 77.2%; Score 553.2; DB 13; Length 726;
 Best Local Similarity 86.4%; Pred. No. 1.1e-146;
 Matches 622; Conservative 0; Mismatches 95; Indels 3; Gaps 1;

QY 1 CAGGTGAAACTGACGACGACCTGAACTGCTGAGGCTTCAAGTAAAGATA 60
 DB 7 CAGGTGAAACTGACGACGACCTGAGGCTGAGCTTGATGCTGGGGCTTCAGTGAAGATG 66

```
QY 61 TCCTGCAAGACTCTGAGANACAAATTCATGTAATACACCATGCACTGGGTGAAGCAGAGC 120
   |||||
DB 67 TCCTGCAAGGCTTCTGGCTACACATTCACACTGATGATGCACTGGGTGAAGCAGAGG 126
QY 121 CATGAAAGACCTTGAAGTGAATGAGATTAATCTTAACATGGTGTACTAACTAC 180
   |||||
DB 127 CTGGAACAAGCCTTGAAGTGAATGAGATTAATCTTGTATAGTTATACCTAGCTAC 186
QY 181 AAGCAAAAGTTCAAGGCAAGGCCACATTAATCTGTAGACAAGTCTCCAGACAGCTTAC 240
   |||||
DB 187 AATCAAAAAGTTCAAGGCAAGGCCACATTAATCTGTAGACAAGTCTCCAGACAGCTTAC 246
QY 241 ATGAGAGTCCGCAAGCCTGACATCTGAGATTTCTGCACTGTAATCTAGCTGTC---AAGAGAT 297
   |||||
DB 247 ATGAGAGTCCGCAAGCCTGACATCTGAGATTTCTGCACTGTAATCTAGCTGTC---AAGAGAGC 306
QY 298 ACTACGATCCGCTTGTCTTCACTGAGTCAAGGAGCAACGAGTCAACGCTCTCTCAGGTGA 357
   |||||
DB 307 TACTATAGCCGATTTGATTACTGGGGGCCAAGGAGCTACGCTCACCGTCTCTCAGGTGA 366
QY 358 GGGGTTCAAGGCGGAGGTGCTCTGGCGGTGGGAGATCGACATCCAGCTCACTAGCTCT 417
   |||||
DB 367 GGGGTTCAAGGCGGAGGTGCTCTGGCGGTGGGAGATCGACATCCAGCTCACTAGCTCT 426
QY 418 CCAGCAATCATGTCGTGATCTCAGAGGAGAGAGGTCCATGACCTGCACTGGAGGAGCTCA 477
   |||||
DB 427 CCAACACCAATGCTGTGATCTCAGAGGAGAGAGGTCCATGACCTGCACTGGAGGAGCTCA 486
QY 478 AGTAAAGTTACATGCACTGCTGACCAAGAGAGAGGTCCATGACCTGCACTGGAGGAGCTCA 537
   |||||
DB 487 AGTAAAGTTACATGCACTGCTGACCAAGAGAGAGGTCCATGACCTGCACTGGAGGAGCTCA 546
QY 538 TATGACATATCCAAATCTGGCTTCTGAGTCTCCGCTCTGCTTCACTGAGTCACTGGAGT 597
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DB 547 TATGACATATCCAAATCTGGCTTCTGAGTCTCCGCTCTGCTTCACTGAGTCACTGGAGT 606
QY 598 ACCTCTTATCTCTCAATCATGAGAGATGAGAGGCTGTAGTGTGCTGCTTATTAATCTGC 657
   |||||
DB 607 ACCTCTTATCTCTCAATCATGAGAGATGAGAGGCTGTAGTGTGCTGCTTATTAATCTGC 666
QY 658 CATCAGCGAGATGATACCCGCTCACGTTGCTGGAGCACAAGTTGAAATPAAACGG 717
   |||||
DB 667 CTGCAAGAGAGATGATACCCGCTCACGTTGCTGGAGCTGGACCAAGCTGAAATPAAACGG 726

RESULT 14
AAZ28963
ID AAZ28963 standard; DNA; 807 BP.
XX
AC AAZ28963;
XX
DT 07-FEB-2000 (first entry)
XX
DE Anti-Hepatitis B surface antigen (4C2) scFv encoding DNA.
XX
KW Anti-Hepatitis B surface antigen (4C2) scFv; single chain Fv;
   light chain constant region; mouse antibody 1C3; mutation; DNA construct;
   ribosome display; replicable mRNA; replication; translation;
   continuous in vitro evolution; CIVE; mutant protein; diagnostic;
   therapeutic property; ds.
XX
OS Homo sapiens.
XX
PN WO958661-A1.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99MO-AU000341.
XX
PR 08-MAY-1998; 98AU-00003445.
XX
PA (DIAT-) DIATECH PTY LTD.
XX
```

```
PI Coia G, Hudson PJ, Illades P, Irving RA;
XX
DR MPI; 2000-039104/03.
XX
PT Continuous in vitro evolution of proteins by mutation, synthesis and
   selection of mRNA.
XX
PS Example 3; Fig 5d; 78bp; English.
XX
CC The present sequence is a DNA encoding anti-hepatitis B surface antigen
   (4C2) scFv. It can be fused upstream of the DNA encoding light chain
   CC constant region of mouse antibody 1C3 or other gene of interest in a DNA
   CC construct, for ribosome display. The DNA construct is generated for
   CC producing replicable mRNA molecules that are used in continuous cyclic
   CC process of replication, mutation, and translation leading to continuous
   CC in vitro evolution (CIVE) of mutant proteins. This method is useful for
   CC generating proteins with improved diagnostic and therapeutic properties
   XX
SQ Sequence 807 BP; 201 A; 207 C; 217 G; 182 T; 0 U; 0 Other;

Query Match 76.4%; Score 547.6; DB 3; Length 807;
Best Local Similarity 85.2%; Pred. No. 4,3e-145;
Matches 610; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 2 AGGTAAATCTGACAGCAGTCAAGGAGCTGAATCTGATGAGCTGAGGCTTCACTGTAAGATAT 61
   |||||
DB 10 ATGTAAAGTTTCAAGAGTCAAGGAGCTGAGCTGATGAGCTGAGGCTTCACTGTAAGATAT 69
QY 62 CCTGCAAGACTTCTGAGANACAAATTCATGTAATACCAATGCACTGGGTGAAGCAGAGCC 121
   |||||
DB 70 CTGCAAGAGGTTCCGGCTACATTCATGATTAATGCTATGATGAGTGGTGAAGCAGAGTC 129
QY 122 ATGGAAGAGCCTTGAAGTGAATTTGAGAGTAAATCTTAACATAGTGTGCTTAACTTACA 181
   |||||
DB 130 ATGCAAGAGTCTAAGTGAATTTGAGAGTAAATCTTAAATCTTGTGTAATCAAACTTACA 189
QY 182 AGCAGAAAGTTCAAGGCAAGGCCACATTAATGCTGTAAGCAAGTCTCTCCAGACAGCTTACA 241
   |||||
DB 190 ACCAGAAAGTTTGAAGGCCCAAGGCCCAATGATGATGAGCAAAATCTCTCAACAGAGCTATT 249
QY 242 TGGAGCTCCGCAAGCTGACATCTGAGATTTGCACTGATTAATCTGTCAGAGATATCA 301
   |||||
DB 250 TGGAACTTGGCAGATTTGACATCTGAGGATTTGCCATCTTAATTAATCTGTGCAAGATGATCG 309
QY 302 CGGTCCGTTTCTTAATCTGAGTCCAAAGGAGCAACGCTTCAAGCTCTCAGGAGGAGCG 361
   |||||
DB 310 ACTGATCTTCAATGCTGTGGGCTCAAGGAGCAACGCTTCAAGCTCTCAGGAGGAGCG 369
QY 362 GTTCAAGCGAGAGTGTGCTGTGGCGGTGGCGGATCGGACATGAGTCACTCACTCACTCCAG 421
   |||||
DB 370 GTTCAAGCGAGAGTGTGCTGTGGCGGTGGCGGATCGGACATGAGTCACTCACTCCAG 429
QY 422 CAATCATGTCGTGATCTCAAGGAGAGAGTCAACATGACCTGCACTGCACTGCACTCAAGTA 481
   |||||
DB 430 CAATCATGTCGTGATCTCAAGGAGAGAGTCAACATGACCTGCACTGCACTGCACTCAAGTA 489
QY 482 TAAAGTAAATGACATCTGTAAGCAAGAGCAAGCAAGTCACTGCACTGCACTGCACTTATG 541
   |||||
DB 490 TCAAGTAAATGACATCTGTAAGCAAGAGCAAGCAAGTCACTGCACTGCACTGCACTTATG 549
QY 542 ACACATCAAACTGAGCTTGTGAGTCCCTGCTGCTTCACTGAGTCACTGAGTCACTGAGAGCT 601
   |||||
DB 550 ACACATCAAACTGAGCTTGTGAGTCCCTGCTGCTTCACTGAGTCACTGAGTCACTGAGAGCT 609
QY 602 CTATATCTCTCAATCAAGCAGAGAGGCTGTAGATCTGCACTTATTAATCTGCACTC 661
   |||||
DB 610 CTCATCTCTCAATCAAGCAGAGGCTGTAGATCTGCACTTATTAATCTGCACTC 669
QY 662 AGCGAGATGATTAACCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
   |||||
DB 670 ACTGAGATGATTAACCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 725
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OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	715	99.7	717	3	US-09-142-974B-1
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3	593.4	82.8	717	4	US-09-473-653-5
4	590.4	82.3	723	4	US-09-581-345-1
5	547.6	76.4	807	4	US-09-674-677-4
6	534.2	74.5	771	4	US-09-526-738A-1
7	534.2	74.5	780	4	US-09-526-738A-3
8	526.4	73.4	714	4	US-09-798-689-22
9	523.8	73.1	894	4	US-09-486-814A-1
10	521.6	72.7	726	2	US-08-553-487A-25
11	517.4	72.2	1797	1	US-08-463-163-2
12	515.8	71.9	719	3	US-08-279-772A-7
13	512.6	71.5	726	2	US-08-902-486-10
14	512.6	71.5	726	2	US-08-553-487A-27
15	507.2	70.7	810	2	US-08-653-507-1
16	504.6	70.4	732	2	US-08-553-487A-19
17	503	70.2	732	2	US-08-553-487A-21
18	501.6	70.0	1679	2	US-08-661-052-15
19	501.6	70.0	1679	3	US-09-188-082-15
20	501.6	70.0	1679	3	US-09-364-088-15
21	501.6	70.0	1679	4	US-09-102-716-15
22	498	69.5	1545	4	US-09-948-004-17
23	487	67.9	738	2	US-08-553-487A-23
24	471	65.7	843	3	US-09-423-439-43
25	471	65.7	1998	3	US-09-423-439-50
26	436.4	60.9	1256	3	US-09-553-498-7
27	436.4	60.9	1256	3	US-09-618-869-7

28	425.6	59.4	786	3	US-08-635-928-31	Sequence 31, Appl
29	424.4	59.2	883	3	US-09-184-658-7	Sequence 7, Appl
30	424.4	59.2	883	4	US-09-504-262D-7	Sequence 7, Appl
31	409.2	57.1	738	2	US-08-956-047-24	Sequence 24, Appl
32	403.2	56.2	777	4	US-10-092-246-7	Sequence 7, Appl
33	403.2	56.2	777	4	US-10-096-246A-7	Sequence 7, Appl
34	400	55.8	777	4	US-10-092-246-5	Sequence 5, Appl
35	400	55.8	777	4	US-10-096-246A-5	Sequence 5, Appl
36	397	55.4	711	2	US-08-190-199A-64	Sequence 64, Appl
37	396.8	55.3	777	4	US-10-092-246-6	Sequence 6, Appl
38	396.8	55.3	777	4	US-10-096-246A-6	Sequence 6, Appl
39	386.8	53.9	708	2	US-08-190-199A-60	Sequence 60, Appl
40	381	53.1	720	3	US-08-800-198-7	Sequence 7, Appl
41	381	53.1	720	3	US-09-296-595-7	Sequence 7, Appl
42	380.2	53.0	777	4	US-10-092-246-4	Sequence 4, Appl
43	380.2	53.0	777	4	US-10-096-246A-4	Sequence 4, Appl
44	377.2	52.6	774	4	US-10-092-246-3	Sequence 3, Appl
45	377.2	52.6	774	4	US-10-096-246A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1	
US-09-142-974B-1	
Sequence 1, Application US/09142974B	
Patent No. 6451995	
GENERAL INFORMATION:	
APPLICANT: Cheung, Nai-Kong V.	
APPLICANT: Larson, Steven M.	
APPLICANT: Guo, Hong-Fen	
APPLICANT: Rivlin, Ken	
APPLICANT: Sadelain, Michel	
TITLE OF INVENTION: Single Chain FV Constructs of Anti-Ganglioside GD2	
FILE REFERENCE: MSK.P-013-USNP	
CURRENT APPLICATION NUMBER: US/09/142,974B	
CURRENT FILING DATE: 1998-09-18	
PRIOR APPLICATION NUMBER: PCT/US97/04427	
PRIOR FILING DATE: 1997-03-20	
PRIOR APPLICATION NUMBER: 60/013,703	
PRIOR FILING DATE: 1996-03-20	
NUMBER OF SEQ ID NOS: 5	
SOFTWARE: PatentIn Ver. 2.1	
SEQ ID NO 1	
LENGTH: 717	
TYPE: DNA	
ORGANISM: Murine	
FEATURE:	
OTHER INFORMATION: 5F11-8cFv	
NAME/KEY: unsure	
LOCATION: (37)	
NAME/KEY: unsure	
LOCATION: (79)	
US-09-142-974B-1	
Qy	1 CAGGTGAAGCTGACGAGCTGAGCACTGAGTGAAGCTGGGGCTTCACTGATAAGTA 60
Db	1 CAGGTGAAGCTGACGAGCTGAGCACTGAGTGAAGCTGGGGCTTCACTGATAAGTA 60
Qy	61 TCCTGCAAGACTTGTGAGNACAATTCATGATACACATGCACTGGGTGAAGCAGAGC 120
Db	61 TCCTGCAAGACTTGTGAGNACAATTCATGATACACATGCACTGGGTGAAGCAGAGC 120
Qy	121 CATGGAAGAGCCCTTGAGTGTGATGAGTATTAATCTTAACATGATGATCTACTAC 180
Db	121 CATGGAAGAGCCCTTGAGTGTGATGAGTATTAATCTTAACATGATGATCTACTAC 180
Qy	181 AAGCAGAAATTCAAGGCGAAGCCACATTCATGCTGACAGAAATCTCAGACAGCCTAC 240

Db 181 AAGCAGAAAGTTCAAGGCGAAGCCAACTGATGATGAGACAAGTCTCCAGACAGAGCTAC 240
Qy 241 ATGAGAGTCCGCGAGCCTGAGATCTGAGAGATTTCTGCACTTATCTGTGCAAGAGATCT 300
Db 241 ATGAGAGTCCGCGAGCCTGAGATCTGAGAGATTTCTGCACTTATCTGTGCAAGAGATCT 300
Qy 301 ACGGTCCCGTTTGCTTACGTGGGTCCAGAGGAGCCAGCTGACCGTCTCTCAGGTTGAGGC 360
Db 301 ACGGTCCCGTTTGCTTACGTGGGTCCAGAGGAGCCAGCTGACCGTCTCTCAGGTTGAGGC 360
Qy 361 GGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCCGAGATCGAGATCTCACTCACTTCCA 420
Db 361 GGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCCGAGATCGAGATCTCACTCACTTCCA 420
Qy 421 GCATCATGTCTGATCTCCAGGGGAGAGAGTCACTGACCTGCACTGCGAGCTCAAGT 480
Db 421 GCATCATGTCTGATCTCCAGGGGAGAGAGTCACTGACCTGCACTGCGAGCTCAAGT 480
Qy 481 ATAAGTTACATGACCTGTAACAGCAGAGAGCTGTCACCTCCCGCAAAAGATGATTTAT 540
Db 481 ATAAGTTACATGACCTGTAACAGCAGAGAGCTGTCACCTCCCGCAAAAGATGATTTAT 540
Qy 541 GACACATCCAAACTGGCTTCTGAGTCCCTGCTCTGCTTCACTGAGCACTGGGCTCTGGAGC 600
Db 541 GACACATCCAAACTGGCTTCTGAGTCCCTGCTCTGCTTCACTGAGCACTGGGCTCTGGAGC 600
Qy 601 TCTTATTTCTCTCAATCAGCAGATGAGGCTGTAGATGCTGCACTTATTTACTGCGAT 660
Db 601 TCTTATTTCTCTCAATCAGCAGATGAGGCTGTAGATGCTGCACTTATTTACTGCGAT 660
Qy 661 CAGCGAGTAGTAACTCCGCTCAAGTTGCTGGGACACAGTTGAGAAATTAACCG 717
Db 661 CAGCGAGTAGTAACTCCGCTCAAGTTGCTGGGACACAGTTGAGAAATTAACCG 717

RESULT 2
US-09-142-974B-3
; Sequence 3, Application US/09142974B
; Patent No. 6451995
; GENERAL INFORMATION:
; APPLICANT: Cheung, Nai-Kong V.
; APPLICANT: Larson, Steven M.
; APPLICANT: Guo, Hong-Fen
; APPLICANT: Rivlin, Ken
; APPLICANT: Sadelain, Michel
; TITLE OF INVENTION: Single Chain FV Constructs of Anti-Ganglioside GD2
; FILE REFERENCE: MSK.P-013-USNP
; CURRENT APPLICATION NUMBER: US/09/142,974B
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PCT/US97/04427
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,703
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: 5P1-scFv-streptavidin
; NAME/KEY: unsure
; LOCATION: (37)
; NAME/KEY: unsure
; LOCATION: (79)
US-09-142-974B-3

Query Match 99.7%; Score 715; DB 3; Length 1176;
Best Local Similarity 100.0%; Prid. No. 4.3e-198;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGTGAAACCTGACAGATCAGAGACTGTAACTGTGTAACCTTGGGCTTCACTGAAGATA 60
Db 1 CAGGTGAAACCTGACAGATCAGAGACTGTAACTGTGTAACCTTGGGCTTCACTGAAGATA 60
Qy 61 TCTGCAAGACTTTCTGAGAACAAATTTCACTGAATACCAATGATCACTGGGTGAAGCAGAC 120
Db 61 TCTGCAAGACTTTCTGAGAACAAATTTCACTGAATACCAATGATCACTGGGTGAAGCAGAC 120
Qy 121 CATGAAAGAGCCTTGAAGGATTTGAGGATTTAAATCTTAACAATGTTGTAATACTAC 180
Db 121 CATGAAAGAGCCTTGAAGGATTTGAGGATTTAAATCTTAACAATGTTGTAATACTAC 180
Qy 181 AAGCAGAAAGTTCAAGGCGAAGCCCAATTGACTGTAGACAAGTCTCCAGCAGAGCTAC 240
Db 181 AAGCAGAAAGTTCAAGGCGAAGCCCAATTGACTGTAGACAAGTCTCCAGCAGAGCTAC 240
Qy 241 ATGAGAGTCCGCGAGCCTGAGATCTGAGAGATTTCTGCACTTATCTGTGCAAGAGATCT 300
Db 241 ATGAGAGTCCGCGAGCCTGAGATCTGAGAGATTTCTGCACTTATCTGTGCAAGAGATCT 300
Qy 301 ACGGTCCCGTTTGCTTACGTGGGTCCAGAGGAGCCAGCTGACCGTCTCTCAGGTGAGGC 360
Db 301 ACGGTCCCGTTTGCTTACGTGGGTCCAGAGGAGCCAGCTGACCGTCTCTCAGGTGAGGC 360
Qy 361 GGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCCGAGATCGAGATCTCACTCACTTCCA 420
Db 361 GGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCCGAGATCGAGATCTCACTCACTTCCA 420
Qy 421 GCATCATGTCTGATCTCCAGGGGAGAGAGTCACTGACCTGCACTGCGAGCTCAAGT 480
Db 421 GCATCATGTCTGATCTCCAGGGGAGAGAGTCACTGACCTGCACTGCGAGCTCAAGT 480
Qy 481 ATAAGTTACATGACCTGTAACAGCAGAGAGCTGTCACCTCCCGCAAAAGATGATTTAT 540
Db 481 ATAAGTTACATGACCTGTAACAGCAGAGAGCTGTCACCTCCCGCAAAAGATGATTTAT 540
Qy 541 GACACATCCAAACTGGCTTCTGAGTCCCTGCTCTGCTTCACTGAGCACTGGGCTCTGGAGC 600
Db 541 GACACATCCAAACTGGCTTCTGAGTCCCTGCTCTGCTTCACTGAGCACTGGGCTCTGGAGC 600
Qy 601 TCTTATTTCTCTCAATCAGCAGATGAGGCTGTAGATGCTGCACTTATTTACTGCGAT 660
Db 601 TCTTATTTCTCTCAATCAGCAGATGAGGCTGTAGATGCTGCACTTATTTACTGCGAT 660
Qy 661 CAGCGAGTAGTAACTCCGCTCAAGTTGCTGGGACACAGTTGAGAAATTAACCG 717
Db 661 CAGCGAGTAGTAACTCCGCTCAAGTTGCTGGGACACAGTTGAGAAATTAACCG 717

RESULT 3
US-09-473-653-5
; Sequence 5, Application US/09473653
; Patent No. 6703015
; GENERAL INFORMATION:
; APPLICANT: Solomon, Bekka
; APPLICANT: Frenkel, Dan
; TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY
; FILE REFERENCE: 00/20785
; CURRENT APPLICATION NUMBER: US/09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 60/152,417
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1..1)
; OTHER INFORMATION: scFv 508f construct
US-09-473-653-5

Query Match 82.8%; Score 593.4; DB 4; Length 717;
Best Local Similarity 90.1%; Pred. No. 9e-163;
Matches 646; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

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Qy 1 CAGGTGAACTGCAGACAGTCAAGACCTGAGTGTGAGGCTTTCAGTGAAGATA 60
Db 1 CAGGTGAACTGCAGACAGTCAAGGCTGAGTGTGAGGCTTTCAGTGAAGATT 60
Qy 61 TCCGTGCAAGACTTCTGAGAACAAATTCAGTAATACACATGACATGCTGGTGAAGAC 120
Db 61 TCCGTGCAAGGCTTCTGCTACACATTCAGTATATGATGACATGCTGGTGAAGAGT 120
Qy 121 CATGAAAGAGCTTGAAGTGAATGAGATTTAATCTTAACATGAGTACTTAACATAC 180
Db 121 CATGAAAGAGCTTGAAGTGAATGAGATTTAATGATTAATGATGATGATGATGAT 180
Qy 181 AAGCAGAACTTCAAGAGGCAAGCCACATTAAGTGAAGAGTCTCCAGACAGCTTAC 240
Db 181 AAGCAGAACTTCAAGAGGCAAGCCACATTAAGTGAAGAGTCTCCAGACAGCTTAT 240
Qy 241 ATGAGACTCCGACCTGACATCTGAGAGATTTGCAAGTCTAATCTGCAAGA--GAT 297
Db 241 ATGAGACTCCGACCTGACATCTGAGAGATTTGCAAGTCTAATCTGCAAGAGGCT 300
Qy 298 ACTAGGCTCCGCTTGTCTTACTGAGTCCAGAGGCAAGGCTCACGCTCTCTCAGTGA 357
Db 301 ACTAGTCTCTACTTGTCTTACTGAGTCCAGAGTCAAGGCTCACGCTCTCTCAGTGA 360
Qy 358 GGCAGCTCAGGCGAGGAGTGTCTGCGGCTGCGGAGTGAAGTGAAGTCACTGAGTCT 417
Db 361 GGCAGCTCAGGCGAGGAGTGTGTGCTGCGGCTGCGGAGTGAAGTGAAGTCACTGAGTCT 420
Qy 418 CCAGCAATCATGTCTGACATCTCCAGGGGAGAGTCAACATGACCTGCAAGTGAAGTCA 477
Db 421 CCAGCAATCATGTCTGACATCTCCAGGGGAGAGTCAACATGACCTGCAAGTGAAGTCA 480
Qy 478 AGTAAGTATCATGACAGTGTGACAGAGAGGCTGACCTCCCAAAAGATGATTT 537
Db 481 AGTAAGTATCATGACAGTGTGACAGAGAGGCTGACCTCCCAAAAGATGATTT 540
Qy 538 TATGACATCATCAAACTGAGTCTTGAAGTCCCTGCTGCTTCACTGAGGAGTGTGAG 597
Db 541 TATGACATCATCAAACTGAGTCTTGAAGTCCCTGCTGCTTCACTGAGGAGTGTGAG 600
Qy 598 ACTCTTATCTCTCAACATGACAGAGAGGCTGTAAGTCTGCCATTAATTAATGCTG 657
Db 601 ACTCTTATCTCTCAACATGACAGAGAGGCTGTAAGTCTGCCATTAATTAATGCTG 660
Qy 658 CATGAGGAGAGTATTAACCGCTGACAGTCTGCTGCTGAGACAGTGAAGATTAATA 714
Db 661 CATGAGGAGAGTATTAACCGCTGACAGTCTGCTGCTGAGAGGAGGCTGAAGATTAATA 717
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RESULT 4
US-09-581-345-1
Sequence 1, Application US/09581345
Patent No. 6809184
GENERAL INFORMATION:
APPLICANT: Pascan, Ira H.
APPLICANT: Chowdhury, Partha S.
APPLICANT: The Government of the United States
APPLICANT: as represented by The Secretary of the
Department of Health and Human Services
TITLE OF INVENTION: Antibodies, including Fv Molecules, and
TITLE OF INVENTION: Immunocongulates Having High Binding Affinity for
FILE REFERENCE: 015280-339100US
CURRENT APPLICATION NUMBER: US/09/581,345
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/067,175
PRIOR FILING DATE: 1997-12-01
PRIOR APPLICATION NUMBER: WO PCT/US98/25270

PRIOR FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 723
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SS scfV
US-09-581-345-1

Query Match 82.3%; Score 590.4; DB 4; Length 723;
Best Local Similarity 89.7%; Pred. No. 6.7e-162;
Matches 646; Conservative 0; Mismatches 68; Indels 6; Gaps 1;

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Qy 1 CAGGTGAACTGCAGACAGTCAAGACCTGAGTGTGAGGCTTTCAGTGAAGATA 60
Db 4 CAGGTGAACTGCAGACAGTCAAGGCTGAGTGTGAGGCTTTCAGTGAAGATT 63
Qy 61 TCCGTGCAAGACTTCTGAGAACAAATTCAGTAATACACATGACATGCTGGTGAAGAC 120
Db 64 TCCGTGCAAGGCTTCTGCTACACATTCAGTATATGATGACATGCTGGTGAAGAGT 123
Qy 121 CATGAAAGAGCTTGAAGTGAATGAGATTTAATCTTAACATGAGTACTTAACATAC 180
Db 124 CATGAAAGAGCTTGAAGTGAATGAGATTTAATGATTAATGATGATGATGATGAT 183
Qy 181 AAGCAGAACTTCAAGAGGCAAGCCACATTAAGTGAAGAGTCTCCAGACAGCTTAC 240
Db 184 AAGCAGAACTTCAAGAGGCAAGCCACATTAAGTGAAGAGTCTCCAGACAGCTTAT 243
Qy 241 ATGAGACTCCGACCTGACATCTGAGAGATTTGCAAGTCTAATCTGCAAGAAGAT 300
Db 244 ATGAGACTCCGACCTGACATCTGAGAGATTTGCAAGTCTAATCTGCAAGAGGCT 303
Qy 301 ACGGTCCG-----TTTGCTTACTGAGTCCAGAGGCAAGGCTCACGCTCTCTCAGT 354
Db 304 TACGACGAGAGGCTTTTGAATGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 363
Qy 355 GAGGCGGCTTCAAGGCGAGGAGTGTCTGCGGCTGCGGAGTGAAGTGAAGTCACTGAGT 414
Db 364 GAGGCGGCTTCAAGGCGGAGGAGTGTGTGCTGCGGCTGCGGAGTGAAGTGAAGTCACTGAGT 423
Qy 415 TCCACAGCAATCATGTCTGACATCTCCAGGGGAGAGTCAACATGACCTGCAAGTGAAGTCA 474
Db 424 TCCACAGCAATCATGTCTGACATCTCCAGGGGAGAGTCAACATGACCTGCAAGTGAAGTCA 483
Qy 475 TCAAGTATTAAGTATCATGACAGTGTGACAGAGAGGCTGACCTCCCAAAAGATGAG 534
Db 484 TCAAGTATTAAGTATCATGACAGTGTGACAGAGAGGCTGACCTCCCAAAAGATGAG 543
Qy 535 ATTTATGACATCATCAAACTGAGTCTTGAAGTCCCTGCTGCTTCACTGAGGAGTGTGAG 594
Db 544 ATTTATGACATCATCAAACTGAGTCTTGAAGTCCAGAGTGTGCTTCACTGAGGAGTGTGAG 603
Qy 595 GGAACCTTATCTCTCAACATGACAGAGAGGCTGTAAGTCTGCCATTAATTAATGCTG 654
Db 604 GGAACCTTATCTCTCAACATGACAGAGAGGCTGTAAGTCTGCCATTAATTAATGCTG 663
Qy 655 TGCCATGACGAGAGTATTAACCGCTGACAGTCTGCTGCTGAGACAGTGAAGATTAATA 714
Db 664 TGCCATGACGAGAGTATTAACCGCTGACAGTCTGCTGCTGAGAGGAGGCTGAAGATTAATA 723
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RESULT 5
US-09-674-677-4
Sequence 4, Application US/09674677
Patent No. 652622
GENERAL INFORMATION:
APPLICANT: Coia, et al.
APPLICANT: CONTINUOUS IN-VITRO EVOLUTION
FILE REFERENCE: 674537-2003
CURRENT APPLICATION NUMBER: US/09/674,677

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: CURRENT FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: PCT/AU99/00341
: PRIOR FILING DATE: 1999-05-07
: PRIOR APPLICATION NUMBER: AU PP3445
: PRIOR FILING DATE: 1998-05-08
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 4
: LENGTH: 807
: TYPE: DNA
: ORGANISM: Homo Sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (1)..(807)
: OTHER INFORMATION: Sequence of the anti-hepatitis surface antigen (4c2) scFv
: Patent No. 6562622
: US-09-674-677-4

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Query Match	76.4%;	Score 547.6;	DB 4;	Length 807;
Best Local Similarity	85.2%;	Pred. No. 2e-149;		
Matches 610; Conservative	0;	Mismatches 106;	Indels 0;	Gaps 0;

QY	2	AGGTGAAATCGACAGAGTGAAGACCGTGAACCTGAGGAGCTTCACTGAAGATAT	61
Db	10	ATGTGAAGCTTCAGAGAGTACGGGCTTGAGCTGTGAAGCCGGGGTCTCACTGAAGATTA	69
QY	62	CCTGCAAGACTTCTGGAMNCAAAATTCATCTGAATACCACTGCATGGGTGAAGAGCC	121
Db	70	CCTGCAAGGGTTCGGCTACACATTCACATCTGATTTATGCTATGCATTTGGGTGAAGAGATC	128
QY	122	ATGGAAGAAGCCCTGAGTGGATTGGAAGGATTAATCCTAACAAGAGTGTCTAATCA	181
Db	130	ATGCCAAGAGCTAGAGTGGATTGACTTAATTAATTAATTCCTTTGGTAATCAAACTACA	188
QY	182	AGCAGAAGTTCAGAGGCAAGGCAACATTTGACTGTGAACAAGTCTCCAGACAAGCTTACA	244
Db	190	ACCAGAAGTTTGAGGCGCAAGGCCAACATGACTGTGACAACATCTCCAAACAAGGTAATT	248
QY	242	TGGAGTCCGCGAGCCGACATCTGAGAGATTCTGCAAGTCTAATTACTGTCCAGAGACTA	301
Db	250	TGGAACTTGACAGATTGAACATCTGAGAGATTCTGCATCTAATTACTGTCCAGAGGTAATCG	309
QY	302	CGGTCCCGTTTGCTTACGTGGGTCCAAAGGACCAAGCTGACGGTCTCTCAGGTGAAGCG	361
Db	310	ACTGTCCTTTCATGTCTGGGGCAAGGACCAAGCTGACGGTCTCTCAGGTGAAGCG	368
QY	362	GTTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATGAGGCTCACTAGTCTCAG	421
Db	370	GTTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATGTGTGACCAACTCTCAG	428
QY	422	CAATCAATGCTGCACTTCCAGGGGGAAGAGTCAACATGACCTGCGAGTGGAGCTCAAGTA	481
Db	430	CAATCAATGCTGCACTTCCAGGGGGAAGAGTCAACATGACCTGCGAGTGGAGCTCAAGT	488
QY	482	TAAATTACATGACCTGTGACAGCAGAGAGCTGTCACTCCCTCCCAAAAGATGATTTATG	541
Db	490	TCAGGTACGTCACCTGTACCAACAGAAAGTCAAGGACCTCCCTCCCAAAAGATGATTTATG	548
QY	542	ACACATCCAAACGTGGCTTCTGGAATCCCTGCTCGCTTCAAGTGGAGTGGGTCTGGAGCT	601
Db	550	ACACATCCAAACGTGGCTTCTGGAATCCCTGCTCGCTTCAAGTGGAGTGGGTCTGGAGCT	608
QY	602	CTTAATCTCTCAATCAGCAGATGGAAGCTGTAGATGTGCACTTAATTAAGTGCATC	661
Db	610	CTCACTCTCTCAATCAGCAGATGGAAGTGGAGTGGAGTGGCACTTAATTAAGTGCAGC	668
QY	662	AGCGAGTGTATACCCGCTCAAGTTCGGTGTCTGGGACACAGTTTGGAAATAAACGG	717
Db	670	ACTGAGTGTATACCCCTCCACGTTCTGGTGTCTGGGACCAAGCTGGAAATAAACGG	725

RESULT 6
US-09-526-738A-1

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: Sequence 1, Application US/09526738A
: Patent No. 6630584
: GENERAL INFORMATION:
: APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
: APPLICANT: LTD.
: TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
: FILE REFERENCE: 1196336
: CURRENT APPLICATION NUMBER: US/09/526,738A
: CURRENT FILING DATE: 2000-03-16
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 771
: TYPE: DNA
: ORGANISM: Humanus
: US-09-526-738A-1

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Query Match	74.5%	Score 534.2;	DB 4;	Length 771;
Best Local Similarity	84.9%	Pred. No. 1.6e-145;		
Matches 609; Conservative	0;	Mismatches 105;	Indels 3;	Gaps 1;

QY	1	CAGGTGAACCTCAGCAGCTGAGAGCACTGAATCGGTGAGAGCTCGGGCTTCAGTGAAGAATA	60
Db	1	CAGGTCAACCTGCACACACTCTGGGGCTGAACTGGCAAAACCTGGGGCTCAGTGAAGAATG	60
QY	61	TCCTGCAGACTTCTGGAGAACAAATTCACTGAAATACCAATGCACTGGTGAAGCAGAGC	120
Db	61	TCCTGCAGACTTCTGGGTGACTACCTTTTAACTGTGCTACGTGAATGAATCGGGTAAACAGAGG	120
QY	121	CATGGAAAAGCCTTGAGTGAATTGAGAGTATTAATCTTAACAATGGTGGTACTTAATAC	180
Db	121	CTGGACAGGGTCTGGAAATGGAATTGGATTAATTAATCTTAACACTGGTATTAATTAATGAC	180
QY	181	AAGCAGAAATTCAAGGGGCAAGGCCCAATTGACTGTAAACAAGTCTTCACGCAAGCCTTAC	240
Db	181	AATCAGAAATTCAAGAGCAAGGCCCAATTGACTGCAACAACAAATCTTCACAGCAGGCTTAC	240
QY	241	ATGGAGCTCCGAGGCTGACATCTGAGGAATTCTGACAGTATTAATCTGTGACAGATACT	300
Db	241	ATGCAACTGAGAGCCTGAACCAATGTGGAATCTTGCAAGTCTTAATTTATTAACAATGGTTAC	300
QY	301	ACGGTCCCGTTTGCTTAATCTGGGATCCAAAGGACCAAGGTCAACCGTCTTCAGGTGAAGGC	360
Db	301	TC---TTAATTTGACTACGGGGCCAAAGGACCAACGGTCAACCGTCTTCAGGTGAGAGC	357
QY	361	GGTTCAAGGGAGGTGGCTCTGGCGGTGGCGGAATCGCAATCAAGGCTCACTCAAGTCCCA	420
Db	358	GGTTCAAGGGAGGTGGCTCTGGCGGTGGCGGAATCGCAATCAAGGCTCACTCAAGTCCCA	417
QY	421	GCATCATGTCTGCATCTCCAGGGGAGAAAGTCAACATGACCTTGCAATGGCAGTCAAGT	480
Db	418	GCATCATGTCTGCATCTCCAGGGGAGAAAGTCAACATTAACCTTGCAATGGCAGTCAAGT	477
QY	481	ATTAAGTTACATGCATCTGGTACAGACGAAAGCCTGTCACTTCCCCAAAAGATGAATTTAT	540
Db	478	GTAAATTAATCATCATCTGGTTCACAGGAAAGCAGAGCACTTCCCAAACTCTGGAATTTCT	537
QY	541	GACACATCCAAACTGGCTTCTGGAAGTCCCTGCTGACTTCAATGGCAGATGGGTCTGGGACC	600
Db	538	AGCACATCCAAACTGGCTTCTGGAAGTCCCTGCTGACTTCAATGGCAGATGGGTCTGGGACC	597
QY	601	TCTTAATCTCTCACAATCAGCAGCATGGAGGCTGTGAATGCTGCACTTATTAATGTCAT	660
Db	598	TCTTAATCTCTCACAATCAGCAGGATGGAAGCTGAATATGCTGCATTTATTAATGTCAG	657
QY	661	CAGCGAGTAATTAACCGCTCAAGTTCGGTCTGGGACACAGTTGGAATTAACCG	717
Db	658	CAAGGAGTAATTAACCGCTCAAGTTCGGGAGGACCAAGTGCATAATTAACCG	714

RESULT 7
US-09-526-738A-3
; Sequence 3, Application US/09526738A

Tue Feb 22 13:21:04 2005

us-10-075-947a-1.rn1

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; Patent No. 6630584
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
; APPLICANT: LTD.
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336
; CURRENT APPLICATION NUMBER: US/09/526,738A
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent version 3.1
; SEQ ID NO 3
; LENGTH: 780
; TYPE: DNA
; ORGANISM: HUMANUS
US-09-526-738A-3

Query Match      74.5%; Score 534.2; DB 4; Length 780;
Best Local Similarity 84.9%; Pred. No. 1.6e-145;
Matches 609; Conservative 0; Mismatches 105; Indels 3; Gaps 1;

QY 1 CAGGTGAAGTTCGACGAGCTGAGACTGAGTGTGAGGCTTGGGGCTTCAGTGAAGTA 60
DB 7 CAGGTCAAGTTCGACGAGCTGAGGCTGAGTGTGAGGCTTGGGGCTTCAGTGAAGTA 66
QY 61 TCCTGCAAGACTTCTGAGAACAAATTCAGTGAATACACCATGACATGAGGTGAGAGAGC 120
DB 67 TCCTGCAAGACTTCTGAGAACAAATTCAGTGAATACACCATGAGTGAAGTGAAGAGG 126
QY 121 CATTGAAAGAGCTTGAAGTGAATGAGGATTAATCTTAACTGATGAGTGAATGATGAC 180
DB 127 CATTGAAAGAGCTTGAAGTGAATGAGGATTAATCTTAACTGATGAGTGAATGATGAC 186
QY 181 AAGCAGAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB 187 AATGAGAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 246
QY 241 ATGAGAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 247 ATGAGAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 306
QY 301 ACGGTCCCGTTTGCTTACCTGAGGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 307 TC--TTATTGTAAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 363
QY 361 GATTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
DB 364 GATTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 423
QY 421 GCAATCATGTCGATCTCCAGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
DB 424 GCAATCATGTCGATCTCCAGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 483
QY 481 ATAAATTACATGACTGGTACACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
DB 484 GTAAATTACATGACTGGTACACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 543
QY 541 GACCATTCAGAACTGGCTTCTGAGAGTCCCTGCTGCTTCACTGAGAGTGGTCTGGAGC 600
DB 544 AGCATTCAGAACTGGCTTCTGAGAGTCCCTGCTGCTTCACTGAGAGTGGTCTGGAGC 603
QY 601 TCTTAATCTCTCAATATCAGAGAGATGAGGCTGAGAGTGTGACATTAATTAATGAGCAT 660
DB 604 TCTTAATCTCTCAATATCAGAGAGATGAGGCTGAGAGTGTGACATTAATTAATGAGCAT 663
QY 661 CAGCGGAGATGATCCCGCTCAGCTTCCGCTGAGGAGGAGGAGGAGGAGGAGGAGG 717
DB 664 CAAAGGAGATGATCCCGCTCAGCTTCCGCTGAGGAGGAGGAGGAGGAGGAGGAGG 720

RESULT 8
US-09-798-689-22
; Sequence 22, Application US/09798689
; Patent No. 6811779
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```
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
; Patent No. 6811779
; CURRENT APPLICATION NUMBER: US/09/798,689
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/401,163
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/967,113
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 08/706,804
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/476,533
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/326,552
; PRIOR FILING DATE: 1994-10-20
; PRIOR APPLICATION NUMBER: 08/196,041
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent ver. 2.1
; SEQ ID NO 22
; LENGTH: 714
; TYPE: DNA
; ORGANISM: Mouse
US-09-798-689-22

Query Match      73.4%; Score 526.4; DB 4; Length 714;
Best Local Similarity 83.5%; Pred. No. 2.9e-143;
Matches 596; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 1 CAGGTGAAGTTCGACGAGCTGAGACTGAGTGTGAGGCTTGGGGCTTCAGTGAAGTA 60
DB 1 CAGGTCAAGTTCGACGAGCTGAGGCTGAGTGTGAGGCTTGGGGCTTCAGTGAAGTA 66
QY 61 TCCTGCAAGACTTCTGAGAACAAATTCAGTGAATACACCATGACATGAGGTGAGAGAGC 120
DB 61 TCCTGCAAGACTTCTGAGAACAAATTCAGTGAATACACCATGAGTGAAGTGAAGAGG 120
QY 121 CATTGAAAGAGCTTGAAGTGAATGAGGATTAATCTTAACTGATGAGTGAATGATGAC 180
DB 121 CATTGAAAGAGCTTGAAGTGAATGAGGATTAATCTTAACTGATGAGTGAATGATGAC 180
QY 181 AAGCAGAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB 181 GCCCGAAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
QY 241 ATGAGAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 241 CTGAGAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
QY 301 ACGGTCCCGTTTGCTTACCTGAGGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 301 GGTGACTACAGAAAGCTTCTGAGAGTCCCTGCTGCTTCACTGAGAGTGGTCTGGAGC 360
QY 361 GATTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
DB 361 GATTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
QY 421 GCAATCATGTCGATCTCCAGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
DB 421 GCAATCATGTCGATCTCCAGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
QY 481 ATAAATTACATGACTGGTACACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
DB 481 GTAAATTACATGACTGGTACACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
QY 541 GACCATTCAGAACTGGCTTCTGAGAGTCCCTGCTGCTTCACTGAGAGTGGTCTGGAGC 600
DB 541 AGCATTCAGAACTGGCTTCTGAGAGTCCCTGCTGCTTCACTGAGAGTGGTCTGGAGC 600
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QY 601 TCTATTCTCTCAACANTCAGCAGCAGAGGCTGTGAAAGTGTGGCACTATTACTGGCAT 660

QY 601 TCTTACTCTCTCAACATCAGCGAATGAGAGGCTGAAGATGCTGCACCTATTACTGGCAG 660

QY 661 CAGCGAGTAGTAACTCCGCTCACTGTTGCGTGTGCGAGCAACAGTTGGAAATAAAA 714

Db 661 CAAAGGAGTGTAACTCCATTCACGTTGCGCTGGGGGACCAAGCTGGAAATAAAA 714

RESULT 9
US-09-48

```

: Sequence 1 Application US/09486814A
: Patent No. 6562599
:
: GENERAL INFORMATION:
: APPLICANT: YAMAMOTO, Masato
: APPLICANT: HAYASHI, No. 656259910
: APPLICANT: YAMAMOTO, Hiroko
: APPLICANT: TODOH, Naoki
: TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS B VIRUS CORE
: TITLE OF INVENTION: PROTEIN, GENE THEREOF, AND THERAPEUTIC AGENT FOR
: TITLE OF INVENTION: HEPATITIS B CONTAINING THESE
: FILE REFERENCE: 0020-4682P
: CURRENT APPLICATION NUMBER: US/09/486,814A
: CURRENT FILING DATE: 2002-06-13
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: patentIn Ver. 2.1
: SEQ ID NO 1
:
: LENGTH: 894
:
: TYPE: DNA
:
: ORGANISM: Mus sp., strain: Balb/c, tissue: spleen
: FEATURE:
: OTHER INFORMATION: Clone: pzeosv1c9
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(891)
: FEATURE:
: OTHER INFORMATION: Identification Method: E
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(111)
: OTHER INFORMATION: Encoding PRE-HV sequence
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (436)..(528)
: OTHER INFORMATION: Encoding a linker sequence
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (838)..(891)
: OTHER INFORMATION: Encoding a TAIL sequence
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(894)
: OTHER INFORMATION: strandedness: double-stranded
:
: US-09-486-814A-1

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Query Match	73.1%;	Score 523.8;	DB 4;	Length 894;
Best Local Similarity	85.6%;	Pred. No. 1.8e-142;		
Matches 624; Conservative	0;	Mismatches 84;	Indels 21;	Gaps 3;

Qy	1	CAGGTGAACTGCAGACAGTCAGGACCTGAACCTGTGTGAGCCCTGGGGCTTCACTGAAGTA	60
Db	118	CAGGTGAACTGCAGACAGTCAGGACCTGAACCTGTGTGAGCCCTGGGGCTTCACTGAAGTA	177
Qy	61	TCCGCGAAGACTTCTGGANACAAATTCATCTGAATACACCATGCACTGGGTGAAGCAGAGC	120
Db	178	TCCGCGAAGACTTCTGGTTCATCTGATTCATCTGAGCTACACATGAAGTGGGTGAAGCAGAGC	233
Qy	121	CATGGAAGAAGCCTTGAGTGGATTTGAGGATATTAATCCAAACAATGTTGTTACTTAATAC	180
Db	238	AATGGAAGAAGCCTTGAGTGGATTTGATATTAATCCTAACAATGTTGTTACTTACGCTAC	297
Qy	181	AAGCAGAAATTCAAGGGCAAGGCCACATTTGACTGTGACAAAGTCTCTCAGACAGCCTAC	240
Db	298	AACCAAGAAATTCAAGGCAAGGCCACATTTGACTGTGACAAATCTCTCAGACAGCCTAC	357

OY	241	ATGAGAGTCGCGAGAGCTGACATCTGAGAGATTCTGAGCTCTATTACTGTGCAAGAGATCT	300
Db	358	ATGCAACTGAGCAGCCTGACATCTGAGAGCTCTGAGCTCTATTACTGTGCAAGA-----	411
OY	301	ACGGTCCCGTTTGCTTACTGAGGGTCCAGAGGAGCAACGGTCAACGGTCTCTCAGGTGAGAGC	360
Db	412	---CTGGAGCTTGACTACTGGGGGCCAAGGAGCACGGTCAACCGTCTCTCAGGTGAGAGC	468
OY	361	GGTTCAAGCGGAGGTGGCTCTGGCGGTGGCGGATCGACATCGAGCTCACTCACTTCCA	420
Db	469	GGTTCAAGCGGAGGTGGCTCTGGCGGTGGCGGATCGACATCGAGCTCACTCACTTCCA	528
OY	421	GCAATCATGTTCTGCACTTCCAGGGGAGAAAGGTCAACCATGACTTGCAGTGGCAGCTCAAGT	480
Db	529	ACCACATGAGCTGCACTCTCCGGGGAGAAAGATCACTATCACTCAGTGCAGCTCAAGT	588
OY	481	ATAG-----TTACATGCACTGATACAGACGAAGGCTGTCACTCTCCCAAAAGATGG	534
Db	589	ATAGTTCCAAATTACTGTGATTGATAGACGAAGGACGAGGATTTCTCCCTTAACTCTTG	648
OY	535	ATTATGACACATCCAAACTGGCTCTTGGAGTCCCTGTGCTTCAAGTGCAGTGGGCTCT	594
Db	649	ATTATTAGACATCAATGCTGCTCTTGTGAATCCAGTCCGCTTCAGTGGCAGTGGGCTCT	708
OY	595	GGGAGCTTATTTCTCTCAATCAGACAGCAATGAGGCTGTAGATGCTGCCATTATTAC	654
Db	709	GGGAGCTTATTTCTCTCAATTGGCAACATGAGAGGCTGAAGATGTTGCCACTTACTAC	768
OY	655	TGCAATCAGGAGATGATTACCGC-----TCACGTTCCGTTGCTGGAGACAGTTGGAA	708
Db	769	TGCACAGAGGTGTAGTATACACAGCAATTTACGTTCCGTTGCTGGAGACAAAGTTGGAA	828
OY	709	ATAAAGCG 717	
Db	829	ATAAAGCG 837	

RESULT 1C
IIS-08-553

0086-0579
Sequence 25, Application US/08553497A
Patent No. 5844093

GENERAL INFORMATION:

APPLICANT: KETTLEBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSON, DETLEF
APPLICANT: ADAN, JAUME
APPLICANT: MITJANS, FRANCESC
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PULATS, JAUME
TITLE OF INVENTION: ANTI-BEGR SINGLE-CHAIN FVS AND ANTI-BEGR
TITLE OR INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZEILANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978

FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: mouse
STRAIN: Balb/c
TISSUE TYPE: splenocytes
IMMEDIATE SOURCE:
CLONE: 5 F 1 (single-chain Fv, heavy, light chain,
CLONE: linker)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..726
US-08-553-497A-25

Query Match 72.7%; Score 521.6; DB 2; Length 726;
Best Local Similarity 84.4%; Pred. No. 7.2e-142;
Matches 613; Conservative 0; Mismatches 101; Indels 12; Gaps 2;

QY 1 CAGGTGAACTGACGAGCTGAGACCTGAACTGTGAGGCTTGGGGCTTTCAGTGAAGATA 60
Db 1 CAGGTGAACTGACGAGCTGAGGCTGAGGCTGAACTGTGAGGCTTGGGGCTTTCAGTGAAGT 60
QY 61 TCCGCAAGACTTCTGGANCAAAATTCATGATACACATGACCTGGGTGAAGACAGC 120
Db 61 TCCGCAAGGCTTCCGCTACACCTTACACGCACTGATGACCTGGGTGAAGACAGG 120
QY 121 CATGAAAGAGCTTGTAGTGTGAGGTATTAATCCTAATGATGATGATTAATCTAC 180
Db 121 GCTGACAAAGGCTTGTAGTGTGAGGTATTAATCCTAATGATGATGATTAATCTAC 180
QY 181 AAGCAAGATTCAAGGCAAGGCAACATTTGATGATGATGATGATGATGATGATGATGAT 240
Db 181 AATGAAATTTCAAGCAAGGCAACATTTGATGATGATGATGATGATGATGATGATGAT 240
QY 241 ATGAGACTCCGCAAGCTGACATCTGAGGATTTCTGATCTTATTTCTGTGCAAG-AGATAC 299
Db 241 ATGCAACTCAAGACCTGACATCTGAGGATTTCTGATCTTATTTCTGTGCAAG-AGATAC 300
QY 300 TACGGTCCG-----TTTGCTTACTGGGTCCAAAGGACCAAGGTCACGCTCC 348
Db 301 TATGATTAACAGGAGGCTTGTAGTGTGAGGTATTAATCCTAATGATGATGATGATGATGAT 360
QY 349 TCAAGTGAAGCGGTTTCAAGCGGAGTGTGCTCTGCGGTGCGGATGCAATCGAGCTC 408
Db 361 TCAAGTGAAGCGGTTTCAAGCGGAGTGTGCTCTGCGGTGCGGATGCAATCGAGCTC 420
QY 409 ACTAAGTCTCCAGCAATCATCTGTCATCTTCAAGGGAAGAGTCCATGATGATGATGAT 468
Db 421 ACCCAAGTCTCCAGCAATCATCTGTCATCTTCAAGGGAAGAGTCCATGATGATGATGAT 480
QY 469 GGCAGCTCAAGTAAAGTTATACATGCACTGATACCAAGCAAGGCTGTCACTCCCCAAA 528

Db 481 GACAGCTCAAGTAAAGTTATACATGCACTGATACCAAGCAAGGCTGTCACTCCCCAGA 540
QY 529 AGATGATTTATGACATCCAAATGAGCTTGTGAGTCCCTGCTCGCTTCAAGTGAAGT 588
Db 541 CTCCTGATTTATGACATCCAAATGAGCTTGTGAGTCCCTGCTCGCTTCAAGTGAAGT 600
QY 589 GGGTCTGGAGCTTCTTATCTCTCAATGACGATGAGGCTGTGATGATGATGATGATGAT 648
Db 601 GGGTCTGGAGCTTCTTATCTCTCAATGACGATGAGGCTGTGATGATGATGATGATGAT 660
QY 649 TATTACTGCCATCAGCGAGTATTAACCGCTCAGTTCGCTGTGAGACACAGTGGAA 708
Db 661 TATTACTGCCATCAGCGAGTATTAACCGCTCAGTTCGCTGTGAGACACAGTGGAA 720
QY 709 ATAAA 714
Db 721 ATAAA 726

RESULT 11
US-08-463-163-2
Sequence 2, Application US/08463163
Patent No. 5696237
GENERAL INFORMATION:
APPLICANT: Fitzgerald, David J.
APPLICANT: Chaudhary, Vijay K.
APPLICANT: Pastan, Ira H.
APPLICANT: Waldmann, Thomas A.
APPLICANT: Queen, Cary L.
TITLE OF INVENTION: Recombinant Antibody-Toxin Fusion Protein
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,163
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/227,227
FILING DATE: 22-JAN-1981
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/911,227
FILING DATE: 24-SEP-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,361
FILING DATE: 21-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,722
FILING DATE: 08-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-12211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1797
OTHER INFORMATION: /product= "Anti-Tac(Fv) -PE40"
US-08-463-163-2

Query Match 72.2%; Score 517.4; DB 1; Length 1797;
Best Local Similarity 83.7%; Pred. No. 1.7e-140;
Matches 597; Conservative 0; Mismatches 113; Indels 3; Gaps 1;

QY 1 CAGGTGAACTGACAGAGCTGAACTGATGAGCTGAGGCTTCAAGAAATA 60
DB 4 CAGGTGACAGCTGACAGAGCTGAGGCTGAACTGCAAAACCTGGGCTCAGTGAAGATG 63
QY 61 TCCTGCAAGACTTCTGGAACAATTCATGTAATACCACTGACTGGGTGAAGCAGAGC 120
DB 64 TCCTGCAAGGCTTCTGCTACACCTTACTAGCTACAGATGACTGGGTAAACAGAGG 123
QY 121 CATGAAAGAGCTTGAAGTGAATTAATCTTAACAATGATGATGTAACCTAC 180
DB 124 CTGGAAGAGGCTTGAATGATGATTAATTAATCTAGCACTGGGTATCTGAATAC 183
QY 181 AAGCAAGATTCAAGGCAAGGCAATGATGATGATGATGATGATGATGATGATGATG 240
DB 184 AATCAAGAGTTCAAGCAAGGCAATGATGATGATGATGATGATGATGATGATGATG 243
QY 241 ATGAGACTCCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 244 ATGCAAGTGAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 303
QY 301 ACGTCCCGTTGCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 304 GGGGTC---TTTACTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 GGTTCAGGCGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 GGTTCAGGCGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 GCAATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 GCAATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 ATAAGTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 481 ATAAGTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 GACACATCCAACTGAGCTTCTGAGATCCTGCTTCTGAGTGGAGTGGTCTGAGACC 600
DB 541 ACCACATCCAACTGAGCTTCTGAGATCCTGCTTCTGAGTGGAGTGGATCTGAGACC 600
QY 601 TCTTATTTCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 601 TCTTATTTCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 661 CACGGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 713
DB 661 CAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 713

RESULT 12
US-08-279-772A-7
Sequence 7, Application US/08279772A
Patent No. 6080560

GENERAL INFORMATION:
APPLICANT: Russell, David R
APPLICANT: Fuller, James T
TITLE OF INVENTION: Method for Producing Antibodies in Plant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Quaries and Brady
STREET: PO Box 2113

CITY: Madison
STATE: WI
COUNTRY: United States of America
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,772A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11-229-9097-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..719
US-08-279-772A-7

Query Match 71.9%; Score 515.8; DB 3; Length 719;
Best Local Similarity 83.6%; Pred. No. 3.5e-140;
Matches 596; Conservative 0; Mismatches 114; Indels 3; Gaps 1;

QY 1 CAGGTGAACTGACAGAGCTGAACTGATGAGCTGAGGCTTCAAGAAATA 60
DB 7 CAGGTGACAGCTGACAGAGCTGAGGCTGAACTGCAAAACCTGGGCTCAGTGAAGATG 66
QY 61 TCCTGCAAGACTTCTGGAACAATTCATGTAATACCACTGACTGGGTGAAGCAGAGC 120
DB 67 TCCTGCAAGGCTTCTGCTACACCTTACTAGCTACAGATGACTGGGTAAACAGAGG 126
QY 121 CATGAAAGAGCTTGAAGTGAATTAATCTTAACAATGATGATGATGATGATGATGATGAT 180
DB 127 CTGGAAGAGGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 186
QY 181 AAGCAAGATTCAAGGCAAGGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 187 AATCAAGATTCAAGCAAGGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 246
QY 241 ATGAGACTCCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 247 ATGCAACTGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 306
QY 301 ACGGTCGCTTCTTACTGAGGCTCAAGGGAACAGGCTGACCGGCTTCTGAGTGGAGGC 360
DB 307 GGGGTC---TTTACTACTGAGGCTCAAGGGAACAGGCTGACCGGCTTCTGAGGAGCGGT 363
QY 361 GGTTCAGGCGAGGCTTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 420
DB 364 GGTTCAGGCGAGGCTTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 423
QY 421 GCAATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 424 GCAATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483
QY 481 ATAAGTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 484 ATAAGTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543
QY 541 GACACATCCAACTGAGCTTCTGAGATCCTGCTTCTGAGTGGAGTGGGCTGAGACC 600

Db 544 ACCACATCAACCTGGCTTCTGGAATCCCTGCTGCTTCAATGAGAGATCTGGAC 603

Qy 601 TCTTATCTCTCAACATCAGACATGAGGCTGTAGATGCTGCCACTTATTATTCGCCAT 660

Db 604 TCTTACTCTCTCAACATCAGGCGATGAGGCTGAGATGCTGCGCACTTATTATTCGCCAT 663

Qy 661 CAGGAGATGATTAACCGCTCAAGCTTGGTGTGGAGACAGTGGAAATAA 713

Db 664 CAAGAGATCTTACCACTACACGTTCCGTTCTGGAGCAACAGCTGAGCTCAA 716

RESULT 13

US-08-902-486-1d

Sequence 10, Application US/08902486

Patent No. 6140075

GENERAL INFORMATION:

APPLICANT: Russel, David R.

APPLICANT: Fuller, James T.

TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND

TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSES: Quarles & Brady

STREET: 1 South Pinckney Street

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/902,486

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 670513.90261

TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-5000

TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 720 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..719

NAME/KEY: CDS

LOCATION: 1..720

US-08-902-486-10

Query Match 71.9%; Score 515.8; DB 3; Length 720;

Best Local Similarity 83.6%; Pred. No. 3.5e-140;

Matches 596; Conservative 0; Mismatches 114; Indels 3; Gaps 1;

Qy 1 CAGGTGAACCTGACAGCTCAGACCTGAACTGTGNAAGCTTGGGGCTTCAAGTAAGATA 60

Db 7 CAGGTTCACGCTTACGAGCTGAGGCTGAACTGGGAAACCTGGGGCTTCAAGTAAGATG 66

Qy 61 TCTTCGCAAGATTTCTGAGNACAATTCCTGATACACATGCACTGGGTGAAGCAGAC 120

Db 67 TCTTCGCAAGGCTTCTGCTACACCTTTAAGCTACAGAGATGCACTGGGTGAAGCAGAG 126

Qy 121 CATGGAAGAGCTTGAAGTGAATGAGATTAATCTTAACAATGTGTACTAATCTAC 180

Db 127 CCTGAGACGAGCTTGGAGATGATTTGATATTTATCTTACACACTGGGTATATGGAATAC 186

Qy 181 AAGCAAGATTTCAAGGCGAAGCCACATTTAGCTGTAGACAAGTCTTCAGACAGCTTAC 240

Db 187 AATCAAGATTTCAAGGCGAAGCCACATTTAGCTGTAGACAAGTCTTCAGACAGCTTAC 246

Qy 241 ATGAGCTCCGACACCTGACATCTGAGAGATTTCTGAGCTTATCTGTGCAAGAGATCT 300

Db 247 ATGCACTGAGACACCTGACATTTTGAAGACTCTGAGCTTATCTGTGCAAGAGAGGG 306

Qy 301 ACGTCCCGTTTGCTACTGGGCTCAAGGAGACACAGGTACCGTCTCTCAGTGGAGGC 360

Db 307 GGGGTC---TTGACTACTGGGCGCAAGGAACACTCTCAGAGCTCTCCGAGGCGGT 363

Qy 361 GGTTCAGGCGAGGTGCTCTGCGGTGGCGGATGGAATGGAATGAGCTCACTCTTCCA 420

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Db 664 CAAGAGATCTTACCACTACACGTTCCGTTCTGGAGCAACAGCTGAGCTCAA 716

RESULT 14

US-08-553-497A-27

Sequence 27, Application US/08553497A

Patent No. 5844093

GENERAL INFORMATION:

APPLICANT: KETTLERBOROUGH, C. A.

APPLICANT: BENDIG, MARY M.

APPLICANT: ANSELL, KEITH H.

APPLICANT: GUSLOW, DETLEF

APPLICANT: ADAM, JAUME

APPLICANT: MITJANS, FRANCESCA

APPLICANT: ROSELL, ELISABET

APPLICANT: BLASCO, FRANCESC

APPLICANT: PIJULATS, JAUME

TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR

TITLE OF INVENTION: ANTIBODIES

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSES: MILLER, WHITE, ZEILANO & BRANIGAN, P.C.

STREET: 2200 CLARENDON BLVD. SUITE 1400

CITY: ARLINGTON

STATE: VA

COUNTRY: US

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/553,497A

FILING DATE: 17-NOV-1995

CLASSIFICATION: 530

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Job time : 150.31 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 22:26:05 : Search time 464.472 Seconds
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9123.970 Million cell updates/sec

Title: US-10-075-947A-1

Perfect score: 717
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	715	99.7	717	15 US-10-075-947A-1	Sequence 1, Appl1
3	715	99.7	1176	15 US-10-075-947A-3	Sequence 3, Appl1
4	593.4	82.8	717	9 US-09-808-037-5	Sequence 5, Appl1
5	593.4	82.8	717	14 US-10-162-889-5	Sequence 5, Appl1
6	593.4	82.8	717	17 US-10-384-788-5	Sequence 5, Appl1
7	593.4	82.8	717	17 US-10-618-856-5	Sequence 5, Appl1
8	574	80.1	726	15 US-10-259-087A-19	Sequence 19, Appl1
9	574	80.1	726	18 US-10-689-006-19	Sequence 19, Appl1
10	561.4	78.3	786	18 US-10-689-006-23	Sequence 23, Appl1
11	553.2	77.2	726	15 US-10-259-087A-17	Sequence 17, Appl1

12	553.2	77.2	726	18 US-10-689-006-17	Sequence 17, Appl1
13	547.6	76.4	807	16 US-10-408-930-4	Sequence 4, Appl1
14	534.2	74.5	771	14 US-10-247-488-1	Sequence 1, Appl1
15	534.2	74.5	780	14 US-10-247-488-3	Sequence 3, Appl1
16	527.8	73.6	720	9 US-09-976-787-30	Sequence 30, Appl1
17	526.4	73.4	714	10 US-09-798-689-22	Sequence 22, Appl1
18	523.2	73.0	714	9 US-09-976-787-11	Sequence 31, Appl1
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21	505.4	70.5	738	18 US-10-661-617-16	Sequence 16, Appl1
22	504	70.3	1673	10 US-09-819-266-27	Sequence 27, Appl1
23	502.8	70.1	1479	18 US-10-682-845-64	Sequence 64, Appl1
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25	502.8	70.1	1479	18 US-10-682-845-72	Sequence 72, Appl1
26	502.8	70.1	1479	18 US-10-682-845-74	Sequence 74, Appl1
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31	501.2	69.9	1241	17 US-10-362-591-1	Sequence 1, Appl1
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34	501.2	69.9	1479	18 US-10-682-845-66	Sequence 66, Appl1
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37	501.2	69.9	1479	18 US-10-682-845-88	Sequence 88, Appl1
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44	463	64.6	1062	15 US-10-295-757-7	Sequence 7, Appl1
45	449.2	62.6	765	14 US-10-013-173-44	Sequence 44, Appl1

ALIGNMENTS

RESULT 1
US-08-940-544-3
Sequence 3, Application US/08940544B
Publication No. US20020018783A1
GENERAL INFORMATION:
APPLICANT: SADRILAIN, MICHEL
APPLICANT: CHEUNG, NAI-KONG V.
APPLICANT: KRAUSE, ANNA
APPLICANT: GUO, HONG-FEN
TITLE OF INVENTION: FUSION PROTEINS OF A SINGLE CHAIN ANTIBODY AND CD28 AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: MSK.P-035-US
CURRENT FILING DATE: 1997-09-30
CURRENT APPLICATION NUMBER: US/08/940.544B
EARLIER FILING DATE: PCT/US97/04427
EARLIER FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 717
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
OTHER INFORMATION: SF11-scFv
FEATURE:
NAME/KEY: unsure
LOCATION: (37)
FEATURE:
NAME/KEY: unsure
LOCATION: (79)
US-08-940-544-3
Query Match 99.7%, Score 715, DB 8, Length 717;
Best Local Similarity 100.0%, Pred. No. 5.9e+228;

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: SP11-scFv
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (37)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (79)
; US-10-075-947A-1

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Best Local Similarity 100.0%; Pred. No. 5,9e-228;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      361 GGTTCAGGCGGAGGTGAGCTCTGGCGGTGGCGGATCGGACATCGAGCTCAGCTCAAGTCTCCA 420
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; Sequence 3, Application US/10075947A
; Publication No. US20030147808A1
; GENERAL INFORMATION:

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RESULT 5

US-10-162-889-5
; Sequence 5, Application US/10162889
; Publication No. US20030077252A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beke
; APPLICANT: HANAN, Eliat
; TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME
; TITLE OF INVENTION: USEFUL IN DIAGNOSING
; FILE REFERENCE: SOLOMON-28
; CURRENT APPLICATION NUMBER: US/10/162,889
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US/09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-162-889-5

Query Match 82.8%; Score 593.4; DB 14; Length 717;
Best Local Similarity 90.1%; Pred. No. 2.6e-187;
Matches 646; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

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US-10-384-788-5
; Sequence 5, Application US/10384788
; Publication No. US20040013647A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beke
; APPLICANT: FRENKEL, Dan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A PLAQUE-FORMING DISEASE
; FILE REFERENCE: SOLOMON-2D.2
; CURRENT APPLICATION NUMBER: US/10/384,788
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 60/371,735
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 09/808,037
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/830,954
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 10/162,889
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/152,417
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/IL00/00518
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-384-788-5

Query Match 82.8%; Score 593.4; DB 17; Length 717;
Best Local Similarity 90.1%; Pred. No. 2.6e-187;
Matches 646; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

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OY 1CAGGCGGAAACCTGACAGAGCTGAGACCTGAACTGGTGTGAGCTGGGGCTTCAGGAAAGATA 60
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OY 61 TCCTGCAAGACTCTTGANANACAAATTCACTGAAATACCATGACATGACTGGGTGAAGACAGAC 120
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Db 421 CDAGCAATCATCTGTCATCTCCAGGGGAGAAAGGTACCATGACCTGCGAGTGGCAGCTCA 480
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Db 481 AGTATAGTTTACATGACATCTGATACCAAGCAAGAGCCGATGTCACCTCCCAAAAAGATGATT 540
OY 538 TATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTGCTTCACTAGTGGCAGTGGGTCTGGG 597
Db 541 TATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTGCTTCACTAGTGGCAGTGGGTCTGGG 600
OY 598 ACCCTTATTTCTCTCAACAATCAGACATGAGAGGCTGTAGATGTGCTGCATTATTACTGC 657
Db 601 ACCCTTATTTCTCTCAACAATCAGACATGAGAGGCTGTAGAGATGTGCTGCATTATTACTGC 660
OY 658 CATCAGCGGAGTAGTTACCCGCTCAAGTTCGGTGTGGGACACAGTTGGAAATATAAA 714
Db 661 CATCAGCGGAGTAGTTATCCCATTTCAAGTTCGGAGGGGGGCCAAGCTGGAATATAAA 717

RESULT 7
US-10-618-856-5
Sequence 5, Application US/10618856
Publication No. US20040052766A1
GENERAL INFORMATION:
APPLICANT: SOLOMON, Beke
APPLICANT: FREMKEL, Dan
TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY
FILE REFERENCE: SOLOMON-2A
CURRENT APPLICATION NUMBER: US/10/618, 856
PRIOR FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: US/09/473, 653A
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: US 60/452, 417
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 717
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(717)

```

```

US-10-618-856-5
Query Match      82.8%; Score 593.4; DB 17; Length 717;
Best Local Similarity 90.1%; Pred. No. 2,6e-187;
Matches 646; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

OY      1 CAGGTGAACATGACACAGTCTGAGACCTGAACTGAGTGMCGCTGGGGCTTCAGTGAAGATA 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1 CAGGTCAACATGCAAGAGTCAGGGGCTGAGCTGTGAGGCTCGGGGTCTCAGTGAAGATT 60

OY      61 TCCTGCAAGACTTCTGGANNAACAAATTCACTAGTAATACACATGCACTGGGTGAAAGACAGC 120
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      61 TCCTGCAAGAGGTTCTGGCTACACATTCATCTAGTAATAGCTATGCACTGGGTGAAAGACAG 120

OY      121 CATGAAAGAGCCTTGAAGTGAATTGAGGTATTAATCTTAACAAATGTSATTAATACTAC 180
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      121 CATGAAAGAGCTGTAGAGTGAATTGAGGTATTAATTAAGTAATTAATACTATGATGCTTAC 180

OY      181 AAGCAAGATTCAGAGGCAAGGCCCATTTGACTGTAGACAAAGTCTCTCCAGACACAGCTAC 240
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      181 AACCAGAAAGTTCAAGGGCAAGGCCCAATATGACTGTAGACAAATCTCCAGACACAGCTTAT 240

OY      241 ATGAGAGTCCGAGGCTGACATCTGAGAGTTCTGAGTCTATTACTGTGCAAGA---GAT 297
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      241 ATGGAAGCTTGGCAAGCTAGCATCTAGAGATTTCGCATCTATTACTGTGCAAGAGGGCT 300

OY      298 ACTACGGTCCCGTTTCTTAAGTCTGAGTCCAAAGGACACGGTCAACGGTCTCTCAGGTGA 357
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      301 ACTATGTCCTTACTTTGACTTAAGTCTGGGGCCAAAGTACACAGGTCAACGGTCTCTCAGGTGA 360

OY      358 GCGGTTAAGCGGAGGAGTGGCTCTTGGCGGTGGCGGATGGAACATGAGCTCACTAGTCT 417
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      361 GCGGTTAAGCGGAGGAGTGGCTCTTGGCGGTGGCGGATGGAACATGAGCTCACTAGTCT 420

OY      418 CCAGCAATCATGTCTGCATCTCCAGAGGAGAAAGTCAACATGACCTGAGGCAAGTCA 477
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      421 CCAGCAATCATGTCTGCATCTCCAGAGGAGAAAGTCAACATGACCTGAGGCAAGTCA 480

OY      478 AGTAAAGTTACATGCACTGTGTACAGAGAAAGCCTGTCACTCCCCAAAAGATGATT 537
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      481 AGTAAAGTTACATGCACTGTGTATCAGAGAAAGCAGGACCTCCCCAAAAGATGATT 540

OY      538 TATGACATCCAAACTGGCTTCTGGAAGTCCCTGCTCGTTCAATGAGCAGTGGGTTGGG 597
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      541 TATGACATCCAAACTGGCTTCTGGAAGTCCCTGCTCGTTCAATGAGCAGTGGGTTGGG 600

OY      598 ACCCTTAATTCCTCCACAATAGCAGCAGATGAGGCTGTAGAGCTGSCCACTTAATCTGC 657
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      601 ACCCTTAATTCCTCCACAATAGCAGCAGATGAGGCTGTAGAGCTGSCCACTTAATCTGC 660

OY      658 CATGACGGAATGATTACCCGCTCAGTTGGGTCTGGGACACAGTTGGAATAA 714
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      661 CATGACGGAATGATTACCCCATTCAGTTCCGAGGGGGGCCAAGCTGGAATAA 717

RESULT 8
US-10-259-087A-19
: Sequence 19, Application US/10259087A
: Publication No. US20030130190A1
: GENERAL INFORMATION:
: APPLICANT: Vanderbilt University
: APPLICANT: Hallahan, Dennis E
: APPLICANT: Ou, Shmian
: TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES
: FILE REFERENCE: 1142/47/2
: CURRENT APPLICATION NUMBER: US/10/259,087A
: CURRENT FILING DATE: 2002-09-27
: PRIOR APPLICATION NUMBER: US 60/328123
: PRIOR FILING DATE: 2001-10-03
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 19
: LENGTH: 726

```

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial antibody ligand number 2
;
; NAME/KEY: CDS
; LOCATION: (1)..(726)
; OTHER INFORMATION:
US-10-259-087A-19
```

```
Query Match      80.1%; Score 574; DB 15; Length 726;
Best Local Similarity 88.2%; Pred. No. 7.9e-181;
Matches 635; Conservative 0; Mismatches 82; Indels 3; Gaps 1;
```

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QY 1 CAGGTGAAGTTCAGCAGTCAAGCCTGAAGCTGGTGAAGCTGGGCTTCAGTGAAGATA 60
DB 7 CAGGTCAAGTTCAGCAGTCAAGCCTGAAGCTGGTGAAGCTGGGCTTCAGTGAAGATA 66
QY 61 TCCTGCAAGACTTCGTGANAACAAATTCAGTGAATACACATGCACTGGGTGAAGCAGAGC 120
DB 67 TCCTGCAAGGCTTCGTGATACACATTCAGTGAATATGATGCACTGGGTGAAGCAGAG 126
QY 121 CATGAAAGAGCTTGAAGTGAATGAGTATTAATCTTAACAATGCTGACTACTACTAC 180
DB 127 CCTGGGCAAGGCTTGAAGTGAATGAGTATTAATCTTAACAATGAGTGAATGACTAC 186
QY 181 AAGCAAGATTCAAGGCAAGGCCACATGACTGTAGACAAGTCTCCAGACAGCCTAC 240
DB 187 AATGAAGATTCAAGGCAAGGCCACATGACTGTAGACAAGTCTCCAGACAGCCTAC 246
QY 241 ATGAGCTCCGACGCTGACATCTGAGAAATTCGACTATTAATCTGTCAGAGA--GAT 297
DB 247 ATGAGCTCCGACGCTGACATCTGAGAAATTCGACTATTAATCTGTCAGAGAATTGGT 306
QY 298 ACTACGCTCCGTTTGTCTTACTGAGTCCAAAGGACACAGCTCACGCTCTCTCAGGTGA 357
DB 307 AACTACGCTGCTTGTGACTACTGAGGACCAAGGACACAGCTCACGCTCTCTCAGGTGA 366
QY 358 GGCAGTTCAGGCGGAGGTGCTGAGGCGTGGCGGATCGGACATCGAGCTCACTCACTCT 417
DB 367 GGCAGTTCAGGCGGAGGTGCTGAGGCGTGGCGGATCGGACATCGAGCTCACTCACTCT 426
QY 418 CCAACAATCAATGCTGATCTCCAGGGGAGAGGTCAACATGACCTGCACTGAGTGAAGTCA 477
DB 427 CCAACAATCAATGCTGATCTCCAGGGGAGAGGTCAACATGACCTGCACTGAGTGAAGTCA 486
QY 478 AGTAAAGTTACATGACCTGATCCAGAGAAAGCTGTCACTCCCAAAAGATGATT 537
DB 487 AGTAAAGTTACATGACCTGATCCAGAGAAAGCTGTCACTCCCAAAAGATGATT 546
QY 538 TATGACATCCAACTGGCTTCGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 597
DB 547 TATGACATCCAACTGGCTTCGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 606
QY 598 ACTCTTATTCCTCAACATCAGCAGATGAGAGCTGATGCTGCTGCTGCTGCTGCTGCTG 657
DB 607 ACTCTTATTCCTCAACATCAGCAGATGAGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 666
QY 658 CATCAGGAGTGAATGATCCGCTCAAGTTCGCTGCTGAGACACATGTTGAATTAACCG 717
DB 667 CAACAGTGAAGTGAATGATCCGCTCAAGTTCGCTGAGAGGAGGAGCAAGCTGGAATTAACCG 726
```

```
RESULT 9
US-10-689-006-19
; Sequence 19, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Mernaght, Raymond
; TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
; FILE REFERENCE: 1242/72
```

```
; CURRENT APPLICATION NUMBER: US/10/689,006
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US 09/914,605
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 10/259,087
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 726
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial antibody ligand number 2
; NAME/KEY: CDS
; LOCATION: (1)..(726)
US-10-689-006-19
```

```
Query Match      80.1%; Score 574; DB 18; Length 726;
Best Local Similarity 88.2%; Pred. No. 7.9e-181;
Matches 635; Conservative 0; Mismatches 82; Indels 3; Gaps 1;
```

```
QY 1 CAGGTGAAGTTCAGCAGTCAAGCCTGAAGCTGGTGAAGCTGGGCTTCAGTGAAGATA 60
DB 7 CAGGTCAAGTTCAGCAGTCAAGCCTGAAGCTGGTGAAGCTGGGCTTCAGTGAAGATA 66
QY 61 TCCTGCAAGACTTCGTGANAACAAATTCAGTGAATACACATGCACTGGGTGAAGCAGAGC 120
DB 67 TCCTGCAAGGCTTCGTGATACACATTCAGTGAATATGATGCACTGGGTGAAGCAGAG 126
QY 121 CATGAAAGAGCTTGAAGTGAATGAGTATTAATCTTAACAATGCTGACTACTACTACTAC 180
DB 127 CCTGGGCAAGGCTTGAAGTGAATGAGTATTAATCTTAACAATGAGTGAATGACTAC 186
QY 181 AAGCAAGATTCAAGGCAAGGCCACATGACTGTAGACAAGTCTCCAGACAGCCTAC 240
DB 187 AATGAAGATTCAAGGCAAGGCCACATGACTGTAGACAAGTCTCCAGACAGCCTAC 246
QY 241 ATGAGCTCCGACGCTGACATCTGAGAAATTCGACTATTAATCTGTCAGAGA---GAT 297
DB 247 ATGAGCTCCGACGCTGACATCTGAGAAATTCGACTATTAATCTGTCAGAGAATTGGT 306
QY 298 ACTACGCTCCGTTTGTCTTACTGAGTCCAAAGGACACAGCTCACGCTCTCTCAGGTGA 357
DB 307 AACTACGCTGCTTGTGACTACTGAGGACCAAGGACACAGCTCACGCTCTCTCAGGTGA 366
QY 358 GGCAGTTCAGGCGGAGGTGCTGAGGCGTGGCGGATCGGACATCGAGCTCACTCACTCT 417
DB 367 GGCAGTTCAGGCGGAGGTGCTGAGGCGTGGCGGATCGGACATCGAGCTCACTCACTCT 426
QY 418 CCAACAATCAATGCTGATCTCCAGGGGAGAGGTCAACATGACCTGCACTGAGTGAAGTCA 477
DB 427 CCAACAATCAATGCTGATCTCCAGGGGAGAGGTCAACATGACCTGCACTGAGTGAAGTCA 486
QY 478 AGTAAAGTTACATGACCTGATCCAGAGAAAGCTGTCACTCCCAAAAGATGATT 537
DB 487 AGTAAAGTTACATGACCTGATCCAGAGAAAGCTGTCACTCCCAAAAGATGATT 546
QY 538 TATGACATCCAACTGGCTTCGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 597
DB 547 TATGACATCCAACTGGCTTCGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 606
QY 598 ACTCTTATTCCTCAACATCAGCAGATGAGAGCTGATGCTGCTGCTGCTGCTGCTGCTG 657
DB 607 ACTCTTATTCCTCAACATCAGCAGATGAGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 666
QY 658 CATCAGGAGTGAATGATCCGCTCAAGTTCGCTGCTGAGACACATGTTGAATTAACCG 717
DB 667 CAACAGTGAAGTGAATGATCCGCTCAAGTTCGCTGAGAGGAGGAGCAAGCTGGAATTAACCG 726
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RESULT 10

US-10-689-006-23
 : Sequence 23, Application US/10689006
 : Publication No. US20040191249A1
 :
 : GENERAL INFORMATION:
 : APPLICANT: Vanderbilt University
 : APPLICANT: Hallahan, Dennis E
 : APPLICANT: Mernaugh, Raymond
 : TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
 : FILE REFERENCE: 1242/72
 : CURRENT APPLICATION NUMBER: US/10/689,006
 : CURRENT FILING DATE: 2003-10-20
 : PRIOR APPLICATION NUMBER: US 09/914,605
 : PRIOR FILING DATE: 2001-08-30
 : PRIOR APPLICATION NUMBER: US 10/259,087
 : PRIOR FILING DATE: 2002-09-27
 : NUMBER OF SEQ ID NOS: 34
 : SOFTWARE: PatentIn version 3.2
 : SEQ ID NO 23
 : LENGTH: 786
 :
 : TYPE: DNA
 : ORGANISM: artificial
 : FEATURE:
 : OTHER INFORMATION: nucleic acid encoding scFv antibody 10A
 : FEATURE: 1
 : NAME/KEY: CDS
 : LOCATION: (1)..(786)
 : US-10-689-006-23

Db 427 CCAACAAACCAATGGCTGATCTCCAGAGAGAGAGTCAACATCACTGCGCGAGCTCA 486
Qy 478 AGTAAATGATTCATGACCTGGTACACAGAGAGCTTCTCCCAAAAGATGATT 537
Db 487 AGGTAAAGTCAATGACCTGGTTCACAGAGAGAGCTTCCCAAAAGCTGATT 546
Qy 538 TATGACATCCAAACCTGGCTTGGAGTCCCTGCTGCTTCACTGAGTGGCTGG 597
Db 547 TATGACATCCAAACCTGGCTTGGAGTCCCTGCTGCTTCACTGAGTGGCTGG 606
Qy 598 ACCCTTATTCCTCACAATCAGCAGCATGAGAGCTGATGCTGACCTTATTCAGC 657
Db 607 ACCCTTATTCCTCACAATCAGCAGCATGAGAGCTGATGCTGACCTTATTCAGC 666
Qy 658 CATGACGAGAGTATCCCGCTCAGCTTGGTGGTGGACACAGTTGAAATPAAACGG 717
Db 667 CTGACAGAGAGTATCCCGCTCAGCTTGGTGGTGGACACAGTTGAAATPAAACGG 726

RESULT 12

US-10-689-006-17
; Sequence 17, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: McNaught, Raymond
; TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
; FILE REFERENCE: 1242/72
; CURRENT APPLICATION NUMBER: US/10/689, 006
; PRIOR FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US 09/914,605
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 10/259,087
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 726
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial antibody ligand number 1
; NAME/KEY: CDS
; LOCATION: (1)..(726)
US-10-689-006-17

Query Match 77.2%; Score 553.2; DB 18; Length 726;
Best Local Similarity 86.4%; Pred. No. 7,1e-174;
Matches 622; Conservative 0; Mismatches 95; Indels 3; Gaps 1;

Qy 1 CAGGTGAATGACGACGAGTCAAGACCTGAACCTGGTGAAGCTGGGGCTTCAAGTGAAGATA 60
Db 7 CAGGTGAATGACGACGAGTCTGGGGCTGAGCTTGTGATGCTGGGGCTTCAAGTGAAGATA 66
Qy 61 TCTTCGAAGACTTCTGGANCAATTCATGTAATCAACATGCTGGGGTGAAGACAGAG 120
Db 67 TCTTCGAAGACTTCTGGCTACACATTCATGTAATCAACATGCTGGGGTGAAGACAGAG 126
Qy 121 CATGGAAGAGCTTGAAGTGAAGTATTAATCTTAACAATGAGTGGTCACTTAATCTAC 180
Db 127 CTTGGAAGAGCTTGAAGTGAAGTATTAATCTTAACAATGAGTGGTCACTTAATCTAC 186
Qy 181 AAGCAGAAGTTCAGAGGCAAGGCAATTCATGTAAGTCAAGTCTCCAGACAGCCTTAC 240
Db 187 AATCAAAAGTTCAGAGGCAAGGCAATTCATGTAAGTCAAGTCTCCAGACAGCCTTAC 246
Qy 241 ATGAGAGCTCCGAGCTGACATCTGAGAGATTCTGCAAGTCTTATTAAGTGC--AAGAGAT 297
Db 247 ATGAGAGCTCCGAGCTGACATCTGAGAGATTCTGCAAGTCTTATTAAGTGC--AAGAGAT 306

Qy 298 ACTACGTCCTCGTTGCTTACTGAGTCCAAAGGACCAACCGTCAACCGTCTCTCAGGTGGA 357
Db 307 TACTATAGGCAATTTGATTACTGGGGCCAAAGGACGTAACGTCACCGTCTCTCAGGTGGA 366
Qy 358 GGGGTTCAAGGCGAGAGTGGCTTGGCGGTCGGATCGGAATCGAGTCACTCACTGCT 417
Db 367 GGGGTTCAAGGCGAGAGTGGCTTGGCGGTCGGATCGGAATCGAGTCACTCACTGCT 426
Qy 418 CCAAGCAATGCTGCACTCTCAGGGGAGAAAGTACCATGACCTCGAGTGGAGCTCA 477
Db 427 CCAACCAATGCTGCACTCTCAGGGGAGAAAGTACCATGACCTCGAGTGGAGCTCA 486
Qy 478 AGTAAATGATTCATGACCTGGTACACAGAGAGCTTCCCAAAAGATGATT 537
Db 487 AGGTAAAGTCAATGACCTGGTTCACAGAGAGAGCTTCCCAAAAGCTGATT 546
Qy 538 TATGACATCCAAACCTGGCTTGGAGTCCCTGCTGCTTCACTGAGTGGCTGG 597
Db 547 TATGACATCCAAACCTGGCTTGGAGTCCCTGCTGCTTCACTGAGTGGCTGG 606
Qy 598 ACCCTTATTCCTCACAATCAGCAGCATGAGAGCTGATGCTGACCTTATTCAGC 657
Db 607 ACCCTTATTCCTCACAATCAGCAGCATGAGAGCTGATGCTGACCTTATTCAGC 666
Qy 658 CATGACGAGAGTATCCCGCTCAGCTTGGTGGTGGACACAGTTGAAATPAAACCG 717
Db 667 CTGACAGAGAGTATCCCGCTCAGCTTGGTGGTGGACACAGTTGAAATPAAACCG 726

RESULT 13

US-10-408-930-4
; Sequence 4, Application US/10408930
; Publication No. US20030170820A1
; GENERAL INFORMATION:
; APPLICANT: Coia, et al.
; TITLE OF INVENTION: CONTINUOUS IN-VITRO EVOLUTION
; FILE REFERENCE: 674537-2003.1
; CURRENT APPLICATION NUMBER: US/10/408,930
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: PCT/AU99/00341
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 09/674,677
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: AU PP3445
; PRIOR FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc.Feature
; LOCATION: (1)..(807)
; OTHER INFORMATION: Sequence of the anti-hepatitis surface antigen (4c2) scFv
US-10-408-930-4

Query Match 76.4%; Score 547.6; DB 16; Length 807;
Best Local Similarity 85.2%; Pred. No. 5,5e-172;
Matches 610; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

Qy 2 AGGTGAATGACGACGAGTCAAGACCTGAACCTGGTGAAGCTGGGGCTTCAAGTGAAGATA 61
Db 10 ATGTGAAGCTTCAGAGGTCAAGGCTGAGAGTGGTGGGCTCGGGGCTCAAGTGAAGATA 69
Qy 62 CTTGGAAGAGCTTGAAGTGAAGTATTAATCTTAACAATGAGTGGTCACTTAATCTAC 121
Db 70 CTTGGAAGAGCTTGAAGTGAAGTATTAATCTTAACAATGAGTGGTCACTTAATCTAC 129
Qy 122 ATGGAAGAGCTTGAAGTGAAGTATTAATCTTAACAATGAGTGGTCACTTAATCTAC 181
Db 130 ATGGAAGAGCTTGAAGTGAAGTATTAATCTTAACAATGAGTGGTCACTTAATCTAC 189

OY	182	ACACAGAACTTCAAGGCGCAAGGCGCAACTTGACTCTGAGCAAGCTCTCAGACAGCCCTACA	241
Db	190	ACCAAGAACTTGAAGGCCAAGGCCACAACTGACTGTAGACAAATCTCCACACAGCGTAATT	249
OY	242	TGAGAGTCCGCAGACCTGACATCTTGAGAGATTCTGCAGTCTATTACTGTGCAGAGATACTA	301
Db	250	TGGAACTTGGCAGATTGGAATCATCTGAGGAAATCTCCACTCTATTACTGTGCAGAGTGATTCG	309
OY	302	cdgtcccgcttgccttactgaggtatcgaaggagacacggatcacccgactctccacaggtgagggcg	361
Db	310	actggtccttccatgctcttggggccaaaggagcacaggctcacccgtctcttcaggtgagggcg	369
OY	352	gttccagggcgaggtggtcttgcgggtggtggcgatcgacatcgagctcactcagttcttcag	421
Db	370	gttccagggcgaggtggtcttgcgggtggtggcgatcgacatcgagctcactcagttcttcag	429
OY	422	caatcatgctctgcatctgcaggggaaagaagtcacatgacnctcagtcagtgagagctcacaagta	481
Db	430	caatcatgctctgcatctgcaggggaaagaagtcacatgacnctcagtcagtgagagctcacaagta	489
OY	482	taagttaacatgcactggtatccacagcagaagcgtctcaactcccccamaaagatggatttatg	541
Db	490	tcagggtacgtgcactggtatccacacagaagtcagcagcactcccccamaaagatggatttatg	549
OY	542	acacatcccaaacttggtcttgcagatccctgctgcttccagtgagcagtgagggtctgggaact	601
Db	550	acacatcccaaacttggtcttgcagatccctgctgcttccagtgagcagtgagggtctgggaact	609
OY	602	cttatattcttcacaaatcacagacatgagagctgttaatgctgcacattattatctgcacatc	661
Db	610	ctcacctcttcacaaatcacagacatgagagctgttaatgctgcacattattatctgcacagc	669
OY	662	adcgagagtaattaccgctcacagtttgcgtgctggagacacagttggaaattaaacgg	717
Db	670	actggagagtaattaccctccacagtttgcgtgctggagacacagttggaaattaaacgg	725

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RESULT 14
US-10-247-488-1
: Sequence 1, Application US/10247488
: Publication No. US20030022244A1
: GENERAL INFORMATION:
: APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH &
: TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
: FILE REFERENCE: 1196336-RAMOT
: CURRENT APPLICATION NUMBER: US/10/247,488
: CURRENT FILING DATE: 2002-09-20
: PRIOR APPLICATION NUMBER: US/09/526,738
: PRIOR FILING DATE: 2000-03-16
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 771
: TYPE: DNA
: ORGANISM: Humaneus
: US-10-247-488-1

```

Query Match	74.5%	Score	534.2	DB	14	Length	771
Best Local Similarity	84.9%	Pred. NO.	1.6e-167				
Matches	609	Conservative	0	Mismatches	105	Indels	3
						Gaps	1

Qy	1	CAGGTGAATCTGACAGCAGCTAGAGAACTTGAATCTGCTGAGGAGCTTCACTGAAGTA	60
Dy	1	CAGGTGAATCTGACAGCAGCTAGAGAACTTGAATCTGCTGAGGAGCTTCACTGAAGTA	60
Qy	1	CAGGTGAATCTGACAGCAGCTAGAGAACTTGAATCTGCTGAGGAGCTTCACTGAAGTA	60
Dy	1	CAGGTGAATCTGACAGCAGCTAGAGAACTTGAATCTGCTGAGGAGCTTCACTGAAGTA	60
Qy	61	TCTCGCAAGACTTCTGAGAACAAATTCTACTGAATACACATGACATCTGGTGAACAGAC	120
Dy	61	TCTCGCAAGACTTCTGAGAACAAATTCTACTGAATACACATGACATCTGGTGAACAGAC	120
Qy	61	TCTCGCAAGACTTCTGAGAACAAATTCTACTGAATACACATGACATCTGGTGAACAGAC	120
Dy	61	TCTCGCAAGACTTCTGAGAACAAATTCTACTGAATACACATGACATCTGGTGAACAGAC	120
Qy	121	CATGAAAGAGCCTTGAGTGAATTTGAGGTATTAATCTCTAACATGGTGTACTAATAC	180
Dy	121	CATGAAAGAGCCTTGAGTGAATTTGAGGTATTAATCTCTAACATGGTGTACTAATAC	180
Qy	121	CATGAAAGAGCCTTGAGTGAATTTGAGGTATTAATCTCTAACATGGTGTACTAATAC	180
Dy	121	CATGAAAGAGCCTTGAGTGAATTTGAGGTATTAATCTCTAACATGGTGTACTAATAC	180

QY	181	AAGCAAGAGTTCAAGGGCAAGGCGCATTTGACTGTAGACAAGCCCTCCAGACAGGCTAC	240
Db	181	AATCAAGAGTTCAAGGACAAAGGCGCATTTGACTGTAGACAAGAAATCTCTCCAGCAGGCGCTAC	240
QY	241	ATGAGAGCTCCGCAAGCTGTGCATCTGAGGATTTGTGCAGTCTATTACTGTGCAAGAGATACT	300
Db	241	ATGCAACTGAGAGGAGCTGTGCAAAATGTGAGCTCTGCAAGTCTATTATTGTCAAACTGGATTAC	300
QY	301	ACGGTCCCGTTTGCTTACTCTAGGGGTCCAAAGGACACAGGTGACCGGTCTCTCAGGTGGAGGC	360
Db	301	TC---TTATTTTGACTACTGAGGGGCCAAAGGACACAGGTGACCGGTCTCTCAGGTGGAGGC	357
QY	361	GGTTTCAGGCGGAGGTGGCTCTTGGCCGATGGCGGATCGACATCGAGCTCACTCAGTCTCCA	420
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QY	421	GCAATCATGTCTGCAATCTCCAAAGGGAGAAAGTTCACATCATGACTCTGCAGTGGCAGCTCAAGT	480
Db	418	GCAATCATGTCTGCAATCTCCAAAGGGAGAAAGTTCACATCATGACTCTGCAGTGGCAGCTCAAGT	477
QY	481	ATAAGTTACATGCACCTGGTATCCAGCAGAGAAGCTGTCACTCCGCCCAAAAGATGAAATTTAT	540
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QY	541	GACACATCCAAACTGGGCTTTCTGGAATCCTCTGCTCGCTTCAATTGCGCAGTGGGCTGTGGAAAC	600
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Db	598	TCTTATTTCTTCACATCAGCAGCAGATGAGGCGTGTAGATGCTGCCACTATTACTGCCAG	657
QY	661	CAGCGGAGTAGTAACTCCCGCTACAGTTCCGCTGCTGGGACACAGTTGGAAATTAACGG	717
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RESULT 15
US-10-247-488-3
? Sequence 3, Application US/10247488
? Publication No. US20030022244A1
? GENERAL INFORMATION:
? APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH &
? TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
? FILE REFERENCE: 1196336-RAMOT
? CURRENT APPLICATION NUMBER: US/10/247,488
? CURRENT FILING DATE: 2002-09-20
? PRIOR APPLICATION NUMBER: US/09/526,738
? PRIOR FILING DATE: 2000-03-16
? NUMBER OF SEQ ID NOS: 8
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 3
? LENGTH: 780
? TYPE: DNA
? ORGANISM: Humanus
US-10-247-488-3

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Query Match	74.5%	Score 534.2	DB 14	Length 780
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Qy	TCTGTCAAGACTTTGTGGAAACAATTCACTGGAATACACATGCACTGGGTGAAGCAGAC	120
Db	TCTGTCAAGACTTTGTGGCTACACCTTTAATAAGCTACGAAAGAACTGGGTAAACAGAGG	126
Qy	CATGAAAGACCTTGTAGTGATTTGAGGATTTAATCTTAACAATGTGTGATTAATACTAC	180
Db	CCTGGAACAGGGTCTGGAATGGAATTGATTAATCAATCTTAACCACTGGTATTAATCAAGTAC	186

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 20:04:30 ; Search time 2571.88 Seconds
(without alignments)
10611.722 Million cell updates/sec

Title: US-10-075-947A-1

Perfect score: 1 caggtggaactgcagcagtc.....cacagtcggaataaacgg 717

Sequence:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_est1:*
2: gb_est2:*
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6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	437.2	61.0	872	7	CK629396 AMO-AA001
2	431.6	60.2	601	5	BQ474958 carabua4g
3	426.6	59.5	1104	7	CK629846 AM2-AA002
4	415	57.9	1419	7	CK629415 AM1-AA001
5	413.6	57.7	1339	7	CK629414 AM1-AA001
6	368.2	51.4	672	7	CK633068 AM3-AP001
7	368.2	51.4	672	7	CK633069 AM3-AP001
8	344.6	48.1	963	7	CK629843 AM2-AA002
9	344	48.0	823	7	CK632348 AM4-AA000
10	336.4	46.9	567	5	BQ328142 MR4-RT004
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12	316.8	44.2	476	2	BF923394 QV4-MT024
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17	301.8	42.1	653	5	BQ321980 MR1-CT073
18	300.2	41.9	565	2	BF801321 MR0-CT002
19	297.2	41.5	544	5	BQ10337 MR0-BT450
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21	293.4	40.9	413	2	BF923369 QV4-MT024
22	293	40.9	403	5	BQ375976 RC3-TN009
23	293	40.9	416	4	BI025870 IL0-MT036
24	293	40.9	419	5	BQ321312 RC0-CT047

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31	293	40.9	449	5	BQ321309
32	293	40.9	449	5	BQ372280
33	293	40.9	454	2	BF836107
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37	293	40.9	459	4	BI025872
38	293	40.9	460	5	BQ321747
39	293	40.9	461	4	BI043087
40	293	40.9	462	4	BI030046
41	293	40.9	464	4	BI043086
42	293	40.9	473	5	BQ321749
43	292	40.7	407	5	BQ328151
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ALIGNMENTS

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LOCUS
DEFINITION AMO-AA0013-110902-011-H03 AA0013 Apis mellifera cDNA, mRNA
ACCESSION CK629396
VERSION CK629396
KEYWORDS
SOURCE CK629396.1 GI:45753871
ORGANISM
EST.
Apis mellifera (honey bee)
Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyrygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apidae; Apib.
1 (bases 1 to 872)

REFERENCE
AUTHORS
Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., pinheiro,D.G.,
Mata,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.P.R.,
Ramos,R.G.P., Reis,L.F.L., Dias Neto,B., Souza,S.J., Simpson,A.J.G.,
Zago,M.A., Soares,A.E.B., Biondi,M.W.G., Espinheiro,E.M.,
Espindola,F.S., Peco-Larson,M.L., Simoes,Z.L.P., Hatfielder,K. and
Silva,W.A., Jr.
Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
Unpublished (2004)
Contact: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Department of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Celso Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br
This sequence was derived from the PAPSP Genome Program
High quality sequence start: 66
High quality sequence stop: 625.

FEATURES

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1..872
/organism="Apis mellifera"
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/sex="female, worker"
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Best Local Similarity 81.8%; Pred. No. 7.4e-118;
Matches 529; Conservative 0; Mismatches 111; Indels 7; Gaps 2;

QY 77 GANCAATTCAGTGAATACCACTGATGCGGTGAAGCAGAGCCATGAAAGACCTTG 136
Db 752 GCTACATCTTCACAGATTATGATATGACCTGGGTGAAGCAGAGCCCTGAAACAGGACTTG 693
QY 137 AGTGAATTTGAGGATTTAATCTTAACAATGGTGTACTTAATCAACAGCAAGTTCAAG 196
Db 692 AGTGAATTTGAGGATTTT-TCCTGAGAGGGAGTACTGAATACATGAGAGTTCAAG 634
QY 197 GCAAGGCCAATGACTGTAGACAGAGTCTTCAGACAGCCTACATGAGTCCGACCC 256
Db 633 GCAAGGCCAATGACTGTAGACAGAGTCTTCAGACAGCCTACATGAGTCCGACCC 574
QY 257 TGACATCTGAGGATTTGCAAGTCTTATTAATCTGTGCAAG-ATACCTAGCTCCCTG 310
Db 573 TGACATCTGAGGATTTGCTGTCTTATTAATCTGTGCTAGAGGGAGTACTATAGGCGTACT 514
QY 311 TTGCTTCTGGGTCCAGAGGACCAAGGTCACCGCTCTCAGAGTGAAGGCGTTCAGAGCG 370
Db 513 TTGCTTCTGGGTCCAGAGGACCAAGGTCACCGCTCTCAGAGTGAAGGCGTTCAGAGCG 454
QY 371 GAGGTGGCTCTGGCGGTGGCGGATCGACATCGAGTCACTCACTCAAGTCTCAAGTCAATGT 430
Db 453 GAGGTGGCTCTGGCGGTGGCGGATCGACATCGAGTCACTCAAGTCTCAAGTCAATGT 394
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Db 393 CTGATATCTCCAGGGGAGAGAGTCAACCATCTGCACTGAGTCAAGTCAAGTCAAGTCA 334
QY 491 TGCACTGCTGACAGAGGCTGTGACCTCCCGCCAAAGATGATTTAAGACACATCCA 550
Db 333 TATATTTGTACCAAGAGAGTGTGATCTCTCCCAACATCTCTGATTTAAGACACATCCA 274
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Db 273 AACTGGCTTCTGAGTCCCTGCTGCTTCAAGTGGCACTGGGAGCTCTTATTTCTC 214
QY 611 TCACATCTGAGGATGAGGCTGTAGATGCTGCACTTATTAATCTGCACTGAGGAGTGA 670
Db 213 TCACATCTGAGGATGAGGCTGTAGATGCTGCACTTATTAATCTGCACTGAGGAGTGA 154
QY 671 GTTACCCGCTCAGCTTGGTGGTGGGACACAGTTGGAATTAACCG 717
Db 153 GTTATCCGTACACCTTGGAGGGGGACCAAGCTGAGCTGAACCG 107

RESULT 2
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LOCUS Carabus9412.b Carabus granulatus cDNA Carabus granulatus cDNA clone
DEFINITION Carabus9412 5', mRNA sequence.
ACCESSION BO474958
VERSION BO474958.1 GI:25957232
KEYWORDS EST.
SOURCE Carabus granulatus
ORGANISM Carabus granulatus
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae; Carabini;
Carabina; Carabus; Carabus.
1 (bases 1 to 601)
Theodorides, K., de Riva, A., Gomez-Zurita, J., Foster, P.G. and
Vogler, A.P.
Comparison of EST libraries from seven beetle species: towards a
framework for phylogenomics of the Coleoptera
Insect Mol. Biol. 11 (5), 467-475 (2003)
JOURNAL MEDLINE
PUBMED 12217875
12230545
Contact: Foster PG
Vogler, Entomology
The Natural History Museum
Cromwell Road, London, SW7 5BD

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Location/Qualifiers
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/organism="Carabus granulatus"
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Matches 501; Conservative 0; Mismatches 89; Indels 6; Gaps 1;

QY 128 AGAGCTTGAAGGATTTGAGGATTTAATCTTAACAATGGTGTACTTAATCAACAGCAGA 187
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QY 188 AGTTCAAGGCAAGGCAATTTGACTGTAGACAGAGTCTTCAGACAGCCTATATGAGC 247
Db 540 AGTTCAAGGCAAGGCAATTTGACTGTAGACAGAGTCTTCAGACAGCCTATATGAGC 481
QY 248 TCCGACGCTGACATCTGAGGATTTCTGAGTCTTATTAATCTGTGCAAG-ATACCTA 301
Db 480 TCACTAGGCTGACATCTGAGGATTTCTGAGTCTTATTAATCTGTGCAAG-ATACCTA 421
QY 302 CGGTCCGTTTCTTACTGAGGATTTCAAGGACCAAGGTCACCGTCTCTCAAGTGAAGCG 361
Db 420 GCGCTTACTTGAATTTGAGGAGGCAAGGACCAAGGTCACCGTCTCTCAAGTGAAGCG 361
QY 362 GTTCAAGGCAAGGCTCTGCGGTGGGATCGGACATCGAGTCACTCAAGTCTCAAGTCT 421
Db 360 GTTCAAGGCAAGGCTCTGCGGTGGGATCGGACATCGAGTCACTCAAGTCTCAAGTCT 301
QY 422 CAATCATCTGATCTGATCTCAAGGAGAGAGTCAACATGACCTGCACTGAGGAGTCAAGT 481
Db 300 CAATCATCTGATCTGATCTCAAGGAGAGAGTCAACATGACCTGCACTGAGGAGTCAAGT 241
QY 482 TAAAGTTAATGACATGATGACAGAGAGGCTGTCACTTCCCAAAAGATGATTTAG 541
Db 240 TAAAGTTAATGATGATGACAGAGAGGCTGTCACTTCCCAAAAGATGATTTAG 181
QY 542 ACAATCAACAACTGGTCTTGAAGTCCCTGCTGCTTCAAGTGGCACTGGGAGTCTGGAACCT 601
Db 180 ACAATCAACAACTGGTCTTGAAGTCCCTGCTGCTTCAAGTGGCACTGGGAGTCTGGAACCT 121
QY 602 CTATTTCTCTCAACATCAAGAGATGAGGCTGTAGATCTGCACTTATTAATCTGCACTC 661
Db 120 CTATTTCTCTCAACATCAAGAGATGAGGCTGTAGATCTGCACTTATTAATCTGCACTC 61
QY 662 AGCGAGTGAATTAACCGCTCAGCTTGGTGGTGGGACACAGTTGGAATTAACCG 717
Db 60 AGTGAAGTGGTGAATTAACCGCTCAGCTTGGTGGGAGGAGGACCAAGCTGAGCTGAACCG 5

RESULT 3
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LOCUS CK629846
DEFINITION AM2-AA0023-091202-021-F02 AA0023 Apis mellifera cDNA, mRNA
sequence.
ACCESSION CK629846
VERSION CK629846.1 GI:45754321
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apoidea; Apis.
1 (bases 1 to 1104)
Nunes, F.M.F., Valente, V., Sousa, J.F., Cunha, M.A.V., Pinheiro, D.G.,
Maia, R.M., Araujo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F.,
Monezi, N., Nascimento, A.M., Peixoto, P.M.V., Silva, M.F.R.,

Ramoa, R. G. P., Reis, L. P. L., Dias Neto, E., Souza, S. J., Simpson, A. J. G., Zago, M. A., Soares, A. E. E., Bitondi, M. M. G., Espinheiro, E. M., Espindola, F. S., Paeo-Larson, M. L., Simoes, Z. L. P., Hartfelder, K. and Silva, W. A. Jr.

TITLE Open reading frame ESTs - an efficient strategy for analysis of the honey bee transcriptome
JOURNAL Unpublished (2004)

Email: wilsonj@uap.br
This sequence was derived from the FAPESP Genome Program
High quality sequence start: 64
High quality sequence stop: 594.

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				Gaps 3

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Qy	540	TGACACATCCAAAGTGGCTTCTGAGTCCCTGCTGCTTCAATGAGCAATGGGCTTGGAGC
Db	267	TGACACATCCAAAGTGGCTCTGGAGTCCCTTTTGCTTCAATGAGCAATGGGCTTGGAGC
Qy	600	CTCTTATTTCTTCAATCAGACAGATGGAAGCTGAATGTCTGCCACTTATTAATCTGCCA
Db	207	CTCTTATTTCTTCAATCAGACAGATGGAAGCTGAATGTCTGCCACTTATTAATCTGCCA

Oy 660 TCACCGAGTAGTTACCCGCTACGTTCCGTGCTGGGACACAGTTGGAAATAAACCG 712
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 Db 147 GGAGTGGAGTGGTTATCCGTACACAGTTCGAG-GGGGACCAAGCTGGAGCTGAAACGG 91

RESULT 4	1419 bp	mRNA	linear	EST 26-MAR-2004
LOCUS	CK629415/c			
DEFINITION	CK629415			
	AM1-AA0014-041102-021-H09 AA0014			
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ACCESSION	CK629415			
VERSION	CK629415.1			
KEYWORDS	GI:45753890			
SOURCE	Est.			
	<i>Apis mellifera</i> (honey bee)			

SOURCE OF ORGANISM
Apis mellifera (honey bee)
Apis mellifera
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
 Apidae; *Apis*.
 1 (bases 1 to 1419)
 Nunes, F. M. F., Valente, V., Sousa, J. F., Cunha, M. A. V., Pinheiro, D. G.,
 AUTHORS

TITLE	Open reading frame ESTs - an efficient strategy for analysis of the
JOURNAL	honey bee transcriptome
COMMENT	Unpublished (2004)
	Contact: Silva Jr, W. A.

This sequence was derived from the FAPESP Genome Program
High quality sequence start: 63
High quality sequence stop: 605.

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QY	108	GGTGAAGCAGAGCCATGAGGAAAAGACCTTGAATGGAGATTAATCTTAACAATGG	167
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QY	228	CAGACAGAGCTCACTTGAGGCTCCGACACTCGACATCTGAGGATTCGTGAGCTTAATCTG	287
Db	585	CAGACAGAGCTTAATGAGGCTCACTAGGCTGACATCTGAGGACTCTGCTGTATTTCTG	526
QY	288	TGCAGAG-----ATTACTACGGTCCGGTTTCTTAATCTGGGTCCAAGGACCAAGGTTAC	341
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Db 465 CGTCTCCTCATGTGAGACCGTTTCAGCGGAGGTGCTCTGTCGTTGCGGATCTGCACAT 406
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Db 405 TGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGATCCCAATGAC 346
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QY 642 TGGCAGTATTAATGTCAGTCAAGGAGAGTATGTTACCCGCTCAGCTTCTGAGAGTGC 701
Db 165 TGGCAGTATTAATGTCAGGAGAGTATGTTACCCGCTCAGTATCCGTACACGTTGAGAGGAGACCA 106
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Db 105 GCTGAGCTGAAACG 91

RESULT 5

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LOCUS AM1-AA0014-041102-021-D05 AA0014 Apis mellifera CDNA, mRNA
DEFINITION sequence.

ACCESSION CK629414
VERSION CK629414.1 GI:45753889
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera

REFERENCE Nunez, F.M.F., Valente, V., Sousa, J.F., Cunha, M.A.V., Pinheiro, D.G.,
Mata, R.M., Araujo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F.,
Monesi, N., Nascimento, A.M., Peixoto, P.M.V., Silva, M.F.R.,
Ramos, R.G.P., Reis, L.F.L., Dias Neto, E., Souza, S.J., Simpson, A.J.G.,
Zago, M.A., Soares, A.E.E., Bitondi, M.M.G., Espresifco, E.M.,
Bepindola, F.S., Paco-larson, M.L., Simoes, Z.L.P., Hartfelder, K. and
Silva, W.A. Jr.

TITLE Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
JOURNAL Unpublished (2004)
COMMENT Molecular Genetic and Bioinformatics Laboratory
Departament of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Celso Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br

FEATURES
source
1..1339
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/sex="female, worker"
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ORIGIN

7

Query Match 57.7%; Score 413.6; DB 7; Length 1339;
Best Local Similarity 82.1%; Pred. No. 8-2e-111;
Matches 514; Conservative 0; Mismatches 104; Indels 8; Gaps 3;

QY 100 ATGCACTGGGTGAAGAGAGCCATGGAAGAGCTTTGAGTGTGG-AGATTATTAATCC 158
Db 715 ATAGCTCGGTGAGCAAGAACGCTTGAACAGGACCTTGAAGTGGAGTCAATTCATTTTTC 656
QY 159 TAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 217
Db 655 TGGAGAGAGAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 596
QY 218 ACAAGTCTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 277
Db 595 ACAAGTCTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 536
QY 278 TCTATTACTGTGCAAGAG-----ATACTACGCTCCGTTTGTCTTACTGTGCTCAAGGA 331
Db 535 TCTATTACTGTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 476
QY 332 CCAAGGTCACCCGTCCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 391
Db 475 CCAAGGTCACCCGTCCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 416
QY 392 GATCGACATGAGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 451
Db 415 GATCGACATGAGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 356
QY 452 TCACCATGACCTGAGTGCAGTCAAGTATTAAGTTACATGCACTGTAACCAAGAGC 511
Db 355 TCACCATGACCTGAGTGCAGTCAAGTATTAAGTTACATGCACTGTAACCAAGAGC 296
QY 512 CTGTACCTCCGCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 571
Db 295 CTGTACCTCCGCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 236
QY 572 CTGTACCTCCGCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 631
Db 235 CTGTACCTCCGCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 176
QY 632 CTGTACCTCCGCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
Db 175 CTGTACCTCCGCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 116
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Db 115 GGGGACCAAGCTGAGCTGAAACGG 90

RESULT 6

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LOCUS AM3-AP0011-151201-021-A08 AP0011 Apis mellifera CDNA, mRNA
DEFINITION sequence.

ACCESSION CK633068
VERSION CK633068.1 GI:45757543
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera

REFERENCE Nunez, F.M.F., Valente, V., Sousa, J.F., Cunha, M.A.V., Pinheiro, D.G.,
Mata, R.M., Araujo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F.,
Monesi, N., Nascimento, A.M., Peixoto, P.M.V., Silva, M.F.R.,
Ramos, R.G.P., Reis, L.F.L., Dias Neto, E., Souza, S.J., Simpson, A.J.G.,
Zago, M.A., Soares, A.E.E., Bitondi, M.M.G., Espresifco, E.M.,
Bepindola, F.S., Paco-larson, M.L., Simoes, Z.L.P., Hartfelder, K. and
Silva, W.A. Jr.

TITLE Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
JOURNAL Unpublished (2004)


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QY 471 CAGCTCAAGATATAGTTATCATGACCTGTTACCGACGAAAGCCCTGTACCTCCCCCAAAAG 530
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DEFINITION
sequence.
ACCESSION CK629843
VERSION CK629843
KEYWORDS EST.
SOURCE CK629843.1 GI:45754318
ORGANISM Apis mellifera (honey bee)
Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apidae; Apis.
REFERENCE 1 (bases 1 to 963)
Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espreafico,E.M.,
Espindola,F.S., Paco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
Silva,W.A. Jr.
Silva,W.A. Jr.
Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
Unpublished (2004)
CONTACT: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Department of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catão Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br
This sequence was derived from the FAPESP Genome Program
High quality sequence start: 88
High quality sequence stop: 376.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
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Best Local Similarity 82.0%; Pred. No. 2e-90;
Matches 460; Conservative 0; Mismatches 89; Indels 12; Gaps 5;

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QY 226 TCCAGACAGCCCTACATGAGAGCTCCGACGCTGCATCATCTGAGATTCGTGACGTCTA-TTA 284
Db 585 TCCAGACAGCCCTATATGAGAGCTCCTACAGCTCATCTGAGAGCTCTGCTGTATTG 526
QY 285 CTGTGCAAGG-----ATACTACGGTCCCTGTTGCTTACTGGGTCCAAAGGACAC-G 336
Db 525 CTGTGCTAGAGGGAGCTACTATAGGGGCTACTTGTGAGCTGTGGGGCTCAAGGGACACGG 466
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QY 337 GTACCGTCTCTCAGAGTGAAGAGCGTTTCAGGCGAGTGGTCTTGGCGGTGGCATCG 396
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QY 397 GACATGAGCTCACTCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAAAGTCACTC 456
Db 405 GACATGAGCTCACTCAGCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGCTCACCC 346
QY 457 ATGACCTGAGTGGAGCTCAAGTATTAAGTTATATGCACATCTGGTACAGAGAGCCTGTC 516
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Db 285 TCTCTCCCAAGACTCCTGATATGATATGACATATCAACATCGTGGCTCTGGAGTCTCTTCCG 226
QY 577 TTCAGTGGAGTGGGTCTGGGACCTTTATTTCTTCACATGACAGCATGAGAGCTGTA 636
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QY 637 GATGCTGCCATTTATTTATCTGCATCAGCGAGTAGTTACCGCTACCGTTGGTGTGG 696
Db 165 GATGCTGCCATTTATTTATCTGCATCAGCGAGTAGTGTATCCGTACACTTCGAGG--GGG 108
QY 697 ACACAGTTGGAATAAACGG 717
Db 107 ACCAAGCTGAGAGCTGAACGG 87

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LOCUS AM0009-070103-021-H02 AM0009 Apis mellifera cDNA, mRNA
DEFINITION
sequence.
ACCESSION CK632348
VERSION CK632348
KEYWORDS EST.
SOURCE CK632348.1 GI:45756823
ORGANISM Apis mellifera (honey bee)
Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apidae; Apis.
REFERENCE 1 (bases 1 to 823)
Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espreafico,E.M.,
Espindola,F.S., Paco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
Silva,W.A. Jr.
Silva,W.A. Jr.
Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
Unpublished (2004)
CONTACT: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Department of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catão Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br
This sequence was derived from the FAPESP Genome Program
High quality sequence start: 70
High quality sequence stop: 545.
FEATURES
Location/Qualifiers
source
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/dev_stage="Mix of adult, pupal, larval and embryonic."
/clone_lib="AM0009"
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 ACCESSION BI030095.1 GI:14436725
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 585)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL0&ct=IL0-MT0355-220301-500-d11&ct3=2001-03-22&ct4=1)
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 High quality sequence stop: 584.
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 /dev_stage="Adult"
 /clone_idb="MT0355"
 /note="Organ: marrow; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 ORIGIN
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 Best Local Similarity 82.2%; Pred. No. 5.5e-86;
 Matches 405; Conservative 0; Mismatches 81; Indels 7; Gaps 2;
 QY 231 CACAGCCTAGATGAGTCCGAGCCGACATCTGAGATTCGCACTTATTAAGTGC 230
 DB 585 CACAGCCAAATGAGTCAACAAGCTACATTCGAGAGCTGCTGCTCAATTTCTGTGC 526
 QY 291 AAGG-----ATTACTAGGTTCCGTTGCTTACTGAGGTCCAGAGGACCAAGCTCCGT 344
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 QY 345 CTCCTCAGTGGAGGCGGTTCAAGCGGAGGTGCTGCGCGTGGCGGATCGACATCGA 404
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 DB 225 CAGTGGGTTGGAGACCTCTTATTTCTGCATATCAGCAGCAGTGAAGGCTGTAGATGCTGC 166
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 DB 106 GGAGCTGAACCG 94
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 LOCUS BF923394
 DEFINITION QV4-NT0248-271100-585-c10 NT0248 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF923394
 VERSION BF923394.1 GI:12319282
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 476)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&ct=QV4-NT0248-271100-585-c10&ct3=2000-11-27&ct4=1)
 Seq primer: puc 18 forward
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 /dev_stage="Adult"
 /clone_idb="NT0248"
 /note="Organ: nervous tumor; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 FEATURES
 source

ORIGIN

Query Match 44.2%; Score 316.8; DB 2; Length 476;
Best Local Similarity 86.0%; Pred. No. 2.8e-82;
Matches 351; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 310 TTTGCTCACTGGGTCAGAGGACCAAGGTCACCTGCTCTCAGTGGAGGGGCTTCAGGC 369
Db 475 TTTGCTCACTGGGTCAGAGGACCAAGGTCACCTGCTCTCAGTGGAGGGGCTTCAGGC 416

Qy 370 GAGAGTGGCTCTGGCGGTGGCGAGTCGACATCGAGTCACTGCTCCAGCAATCATG 429
Db 415 GAGAGTGGCTCTGGCGGTGGCGAGTCGACATCGAGTCACTGCTCCAGCAATCATG 356

Qy 430 TCTGCATCTCCAGGGGAGAAAGTACCATGACTCTGCACTGAGTCAAGTATTAAGTTAC 489
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Qy 550 AAACCTGCTCTGGAGTCCCTGCTGCTGCTGAGTGGAGTGGAGCTCTTATCT 609
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Qy 610 CTTCATCTCAGAGCATGAGAGGCTGTGATGCTGCTCACTTATTACTGCAATCAGGAGT 669
Db 175 CTTCATCTCAGAGCATGAGAGGCTGTGATGCTGCTCACTTATTACTGCAATCAGGAGT 116

Qy 670 AGTACCCGCTGACGCTCGGTGCTGGGACACAGTTGGAATTAACCG 717
Db 115 GATTATCTGACAGCTTGGAGGGGAGACCAAGCTGAGCTGAACCG 68

RESULT 13
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ACCESSION BF857861 GI:12245605
VERSION BF857861.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 498)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
CONTACT: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml.pl?fl=QV1&ct2=QV1-FT0202-
071100-465-g03&ct3=2000-11-07&ct4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 497.

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/clone_id="FT0202"
/note="Organ: prostate tumor; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 44.0%; Score 315.8; DB 2; Length 498;
Best Local Similarity 87.0%; Pred. No. 5.6e-82;
Matches 347; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 319 TGGGTCCAAAGGACCAAGCTCACCCTCTCTCAGTGGAGGGGCTGAGGGGCTG 378
Db 495 TGGGGCCAAAGGACCAAGCTCACCCTCTCTCAGTGGAGGGGCTGAGGGGCTG 436

Qy 379 TCTGGCGGTGGCGATGCAATGAGCTCACTCACTCCAGCAATCATGTCATCT 438
Db 435 TCTGGCGATGGCGATGCAATGAGCTCACTCACTCCAGCAATCATGTCATCT 376

Qy 439 CCAAGGGAGAGGTGACCATGACCTGAGTGGAGCTCAAGTATTAAGTACATGCACTGG 498
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Qy 499 TACCAAGAGAGCTGTCACCTCCCCAAAGATGATTTATGACATCAACATGGCT 558
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Db 255 CTGAGATCCCTTTTCTGCTTCAATGAGGATGGCTGGAGCTTATTTCTTCACATC 196

Qy 619 AGCAGCATGAGAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 678
Db 195 AACCGAATGAGAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 136

Qy 679 CTACGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
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RESULT 14
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LOCUS QV1-FT0202-071100-465-f03 FT0202 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF857860
VERSION BF857860.1 GI:12245604
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 488)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
CONTACT: Simpson A.J.G.

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV1&t2=QV1-PT0202-
071100-465-f03&t3=2000-11-07&t4=1)
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FEATURES
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/clone_11b="PT0202"
/note="Organ: prostate tumor; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 43.7%; Score 313; DB 2; Length 488;
Best Local Similarity 87.3%; Pred. No. 3.7e-81;
Matches 343; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 325 CAAAGGACCAAGCTCCTCTCTCAAGTGGAGGCGGTTCAGGCGAGGTGCTCTGCG 384
DB 488 CAAAGGACCAAGCTCCTCTCTCTCAAGTGGAGTGGCTTCAGGCGAGGTGCTCTGCG 429
QY 385 GGTGGGAGTCCGACATTCGAGCTCACTGCTCCGACATCATGCTGATCTCCAGG 444
DB 428 GATGGGAGTCCGACATTCGAGCTCACTGCTCCGACATCATGCTGATCTCCAGG 369
QY 445 GAGAAAGTCAACATGACCTGACAGTGGAGCTCAAGTAAAGTATGACATGACCTGTAACAG 504
DB 368 GAGAGGCTCAACATGACCTGACAGTGGAGCTCAAGTAAAGTATGACATGACCTGTAACAG 309
QY 505 CAGAAAGTCAACATGACCTGACAGTGGAGCTCAAGTAAAGTATGACATGACCTGTAACAG 564
DB 308 CAGAAAGTCAACATGACCTGACAGTGGAGCTCAAGTAAAGTATGACATGACCTGTAACAG 249
QY 565 GTCCCTGCTGCTTCAAGTGGAGTGGGTCTGGAGACCTCTTATCTCTCAACATCAGACAG 624
DB 248 GTCCCTGCTGCTTCAAGTGGAGTGGGTCTGGAGACCTCTTATCTCTCAACATCAGACAG 189
QY 625 ATGAGAGCTGATAGCTGACCTTATTAATGACATGACAGGAGTAACTCCGCTCAG 684
DB 188 ATGAGAGCTGATAGCTGACCTTATTAATGACATGACAGGAGTAACTCCGCTCAG 129
QY 685 TTCGCTGCTGGAACAAGTGAATPAAACGG 717
DB 128 TTCGAGAGGAGGACCAAGCTGAGTGAACGG 96

RESULT 15
B0373705/c 427 bp mRNA linear EST 21-MAY-2002
LOCUS B0373705
DEFINITION QV1-FT0170-040700-265-b10 FT0170 Homo sapiens cDNA, mRNA sequence.
ACCESSION B0373705
VERSION B0373705.1 GI:21049219
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
1 (bases 1 to 427)
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS
Dias Neto E., Garcia Correa R., Varjowski-Almeida S., Briones M.,
Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F.,
Goldman G.H., Carvalho A.F., Matsukuma A., Bala G.S., Simpson D.H.,
Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V.,
O'Hare M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and
Simpson A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV1&t2=QV1-PT0170-
040700-265-b10&t3=2000-07-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 426.
Location/Qualifiers
1. .427

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_11b="PT0170"
/note="Organ: prostate tumor; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 42.9%; Score 307.8; DB 5; Length 427;
Best Local Similarity 85.9%; Pred. No. 1.2e-79;
Matches 367; Conservative 0; Mismatches 52; Indels 8; Gaps 2;
QY 220 AAGTCTCCAGACAGCTTACATGAGCTCCGAGCTTACATCTGAGATTCTGCAATC 279
DB 427 AAGTCTCCAGACAGCTTACATGAGCTCCGAGCTTACATCTGAGATTCTGCTGTC 368
QY 280 TATTACTGTGCAAGAG-----ATACTAGGTCCTGCTTCTTACTGCTGCTCAAGGACC 333
DB 367 TATTCTGTGCTAGAGGAGCTAATAAGGCTCTTACTGCTGCTGCTCAAGGACC 308
QY 334 AAGGT--CAGGCTCCTGAGTGGAGGCGGTTCAGGAGGAGTGGCTGCGGAGGCG 391
DB 307 AAGGTCAACCGCTCTCTATGAGGCGGCTTCAGGAGGAGTGGCTGCGGAGGCG 248
QY 392 GATCGACATCGAGCTCACTCACTCCAGCATATGCTCATCTCCAGGAGGAGAG 451
DB 247 GATCTGACATTAAGCTCAACCGATCTCCAGCATATGCTCATCTCCAGGAGGAGAG 188
QY 452 TCACCATGACCTGACAGTGGAGCTCAAGTATTAAGTTCATGACAGTGGTCCAGCAGAAC 511
DB 187 TCACCATGACCTGACAGTGGAGCTCAAGTATTAAGTTCATGACAGTGGTCCAGCAGAAC 128
QY 512 CTGTACACCTCCCAAAAGATTAAGACATCAACCTGGCTTGGAGTCCCTG 571
DB 127 CTGTATCTCCCGCAGACTCTGATTTATGACATCAACCTGGCTTGGAGTCCCTG 68
QY 572 CTGTCTCAGTGGAGTGGAGCTCTTATTTCTTCAACATCAGACAGATGAGG 631

Db 67 TTGGCTTCAGTGGCAGTGGGTCTGGGACCTCTTATTCTCTCACAATCAACCGAATGGAGG 8

Oy 632 CTGTAGA 638

Db 7 CTGAGGA 1

Search completed: February 18, 2005, 23:51:41
Job time : 2576.88 secs

QY	24	GAAGACCTGGAGAGTTTATTTCTGTCAGACGAGATTATAGCTGCTCGAGAGGGGGGACCAAG	300
Db	241	GAAGACCTGGAGAGTTTATTTCTGTCAGACGAGATTATTAAGCTGCTCGAGAGGGGGGACCAAG	300
QY	301	CTGGAAATTAAGGTGAGGCGGTTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATTCGAG	360
Db	301	CTGGAAATTAAGGTGAGGCGGTTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATTCGAG	360
QY	361	GTGAGAGTGGAAGAGTCAGGACCTGGCTGGTGGCGCCTTACAGAGGCTTGCATCACT	420
Db	361	GTGAGAGTGGAAGAGTCAGGACCTGGCTGGTGGCGCCTTACAGAGGCTTGCATCACT	420
QY	421	TGCATGCTCTCTGGGGTTTTCATTAAACCAATTATGGTGAACATGGGGTTGCGCAGGCTTCA	480
Db	421	TGCATGCTCTCTGGGGTTTTCATTAAACCAATTATGGTGAACATGGGGTTGCGCAGGCTTCA	480
QY	481	GGAAGGGTCTGAGTGGCTGGAGATATATGGGCTGGTGAAGCAACAATTATTAATTCG	540
Db	481	GGAAGGGTCTGAGTGGCTGGAGATATATGGGCTGGTGAAGCAACAATTATTAATTCG	540
QY	541	GCTTTATATGTCACACTGAGCATCAGCAAGGACAACCTCAAGAGCCAAAGTTTCTTTAA	600
Db	541	GCTTTATATGTCACACTGAGCATCAGCAAGGACAACCTCAAGAGCCAAAGTTTCTTTAA	600
QY	601	ATGAACAGTCTGCAAACTGATGACACAGCCATGTACTACTGTGCCAGTTCGGGGGGTAAAC	660
Db	601	ATGAACAGTCTGCAAACTGATGACACAGCCATGTACTACTGTGCCAGTTCGGGGGGTAAAC	660
QY	661	TACGGCTATGCTTTGGACTACTGGGGTCAAGAACTCAAGTCAACGCTCTCTCTCA	714
Db	661	TACGGCTATGCTTTGGACTACTGGGGTCAAGAACTCAAGTCAACGCTCTCTCTCA	714

Db	181	GCCTTCACTGCGAAGTGAATATGGGACGGAAATTTCACCTTCAACCATCAGACTGTGCAAGCT	240
Qy	241	GAAGACTCTGGCAGTTTATTTCTGTGACAGAGATTATAGCTGTGCGAGGGGGGACCAAG	300
Db	241	GAAGACCTTGGCAGTTTATTTCTGTGACAGAGATTATAGCTGTGCGAGGGGGGACCAAG	300
Qy	301	CTGGAATTAATAAGGTGAGCGCGTTTCAGCGCGAGAGTGGCTCTGCGCGGTGCGGATTCGAG	360
Db	301	CTGGAATTAATAAGGTGAGCGCGTTTCAGCGCGAGAGTGGCTCTGCGCGGTGCGGATTCGAG	360
Qy	361	GTCGAGGTGAAGAGTCAAGACTTGGCTGTGTGGCGCCCTCACAAGACTGTTCATCACT	420
Db	361	GTCGAGGTGAAGAGTCAAGACTTGGCTGTGTGGCGCCCTCACAAGACTGTTCATCACT	420
Qy	421	TGCACGTCTCTGGGTTTTTCAATTAACCAATTAATGCTGTACACTGGGTTTGGCAGCTTCCA	480
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Qy	481	GGAAGGGTCTGAGTGGCTTGGAGTAATATGGGCTGGTGGAGCACAAATTAATTAATTCG	540
Db	481	GGAAGGGTCTGAGTGGCTTGGAGTAATATGGGCTGGTGGAGCACAAATTAATTAATTCG	540
Qy	541	GCCTTTATATGCCAGCTGAGCATAGCAAGGACAACTCCAAAGCCAAAGTTTCTTTAA	600
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Qy	601	ATGAACAGTCTGCAAACTGATGACACAGCCATGTACTACTGTGCAAGTCGGGGGGGTAAAC	660
Db	601	ATGAACAGTCTGCAAACTGATGACACAGCCATGTACTACTGTGCAAGTCGGGGGGGTAAAC	660
Qy	661	TACGGCTATGCTTTGACCTACTGCGGGGTCAAGGAACCTCAAGTCAACCGTCTCTCA	714
Db	661	TACGGCTATGCTTTGACCTACTGCGGGGTCAAGGAACCTCAAGTCAACCGTCTCTCA	714

	RESULT 2				
	AR231457				
LOCUS	AR231457	1173 bp	DNA	linear	PAT 20-DEC-2002
DEFINITION	Sequence 4 from patent US 6451995.				
ACCESSION	AR231457				
VERSION	AR231457.1	GI:27272559			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1173)				
TITLE	Cheung,N.-K.V., Larson,S.M., Guo,H.-F., Rivlin,K. and Sadelain,M. Single chain Fv polynucleotide or peptide constructs of anti-ganglioside GD2 antibodies, cells expressing same and related methods				
JOURNAL	Patent: US 6451995-A 4 17-SEP-2002;				
FEATURES	Location/Qualifiers				
source	1..1173				
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	/mol_type="genomic DNA"				
ORIGIN					
Query Match	100.0%; Score 714; DB 6; Length 1173;				
Best Local Similarity	100.0%; Pred. No.8.8e-179;				
Matches 714; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
OY	1 AGATTGTGATGATGCCAGACTCCCAAAATTCCTGTTGTATCAGCAGAGACAGGGTTACC 60				
Db	1 AGRATTGTGATGATGCCAGACTCCCAAAATTCCTGTTGTATCAGCAGAGACAGGGTTACC 60				
OY	61 ATTAACCTGCAGAAGCGCAGTCAAGTGTCAGTATGATGATGTCGTTGGTATCAACAAGAGCCA 120				
Db	61 ATTAACCTGCAGAAGCGCAGTCAAGTGTCAGTATGATGATGTCGTTGGTATCAACAAGAGCCA 120				
OY	121 GGGCAGTCTCCGAATACTGCTGATATTAATCTTGCAATTCGCTACACTGAGTCCCTGAT 180				
Db	121 GGGCAGTCTCCGAATACTGCTGATATTAATCTTGCAATTCGCTACACTGAGTCCCTGAT 180				
OY	181 CGCTTCACTGGCAATGATATATGGACGGAATTCACCTTCACCATTCAGACTGTGAAGCT 240				
Db	181 CGCTTCACTGGCAATGATATATGGACGGAATTCACCTTCACCATTCAGACTGTGAAGCT 240				

RESULT 3				
BD222935				
LOCUS	BD222935	1371 bp	DNA	linear
DEFINITION	Heteromimboides.			
ACCESSION	BD222935			
VERSION	BD222935.1	GI:3032705		
KEYWORDS	JP 2002521053-A/29.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 1371)			
TITLE	Kiefer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and Zettl,F.			
JOURNAL	Heteromimboides			
	Patent : JP 2002521053-A 29 16-JUL-2002;			
	MICROMET AG			
COMMENT	OS Homo sapiens (human)			
	ON Mus musculus (mouse)			
	PN JP 2002521053-A/29			
	PD 16-JUL-2002			
	PF 28-JUL-1999 JP 2000562401			
	PR 28-JUL-1998 EP 98114082.5			
	PI PETER KIEFER, TORSTEN DREIER, PATRICK A BAEUERLE, KATRIN BOSCHERT,			
	PI FLORIAN ZETTL			
	PC C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,			
	PC C07K19/00,			
	PC C12N5/10,C12P21/02,G01N33/53,G01N33/53//C12N5/10,C12R1:91),			
	PC (C12P21/02,C12R1:91),C12N15/00,C12N5/00,A61K37/02,A61K37/66,			
	PC (C12N5/00,C12R1:91)			
	CC Heteromimboides			
	FH Key			
	FT CDS			
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source	1..1371			
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DEFINITION	Heteromnibodies.					
VERSION	BD222936.1					
KEYWORDS	JP 2002521053-A/30.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
TITLE	Kufner,P., Dreier,T., Beuerle,P.A., Borschert,K. and Zettl,F.					
JOURNAL	Heteromnibodies					
COMMENT	Patent: JP 2002521053-A 30 16-JUL-2002; MICROWET AG					
OS	Homo sapiens (human)					
SN	Mus musculus (mouse)					
PN	JP 2002521053-A/30					
PD	16-JUL-2002					
PF	28-JUL-1999 JP 2000562401					
PI	28-JUL-1998 EP 98114082.5					
BORSCHEKT,	PETER KUFNER, TORSTEN DREIER, PATRICK A BEUERLE, KATRIN					
PC	FLORIAN ZETTL					
PC	C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,					
PC	C07K19/00,					
PC	C12N5/10,C12P21/02,G01N33/53,G01N33/53//C12N5/10,C12R1:91),					
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Best Local Similarity	81.5%; Pred. No.4.8e-116;					
Matches	585; Conservative 0; Mismatches 115; Indels 18; Gaps 2;					
OY	3 TATTGTGATGACCGAGACTCCCAATTCCTGCTGATACAGACAGAGGTTAACCAT	62				
DB	69 TATCCAGCTGAGCCAGCTCCAATAATTCATGTCACATCAGTAGGAGAAGGGTACGCCT	128				
OY	63 AACCTGCAGAGGCATCTCAGAGTGACAGTAATGAATGTGGCTTGATGCCAACAGAAACGAG	122				
DB	129 CACCTGCAGAGGCATCTCAGAGTGACAGTAATGAATGTGGCTTGATGCCAACAGAAACGAG	188				
OY	123 GCAGTCTCCGAACTGCTGATATATCTCTGCATCCAAATGCTACACTGAGTCCCTGATCG	182				
DB	189 GCAATCTCTTAAAGACATGATTTATCTGGGACATCTCACGGATACAGTGAAGTCCCTGATCG	248				
OY	183 CTTCACCTGCAGTGAATATGGGACGGAATTTCACTTTCACATCAGCACTGTGACAGGCTGA	242				
DB	249 CTTTCACAGCAGTGTGATCTGGGACAGATTTTCACTTTCACATCAGCAATGTGACAGTCTGA	308				
OY	243 AGACCTGCAGTGTATTTCTGTGACAGCAGATTAATAGCT-----CGCTCGAGAGGGGG	293				
DB	309 AGACTTGGCAGAGTATTTCTGTGACAGCAGATTAATAGCT-----CGCTCGAGAGGGGG	368				
OY	294 GACCAAGCTGGAATTAATTAAGGTGAGGCGGCTTCACGCGAGAGTGGCTTGGCGGTGGCGG	353				
DB	369 GACCAAGCTGGAATTAATTAAGGTGAGGCGGCTTCACGCGAGAGTGGCTTGGCGGTGGCGG	428				
OY	354 ATCGCAGGTGACAGTGAAGAGATCAGACCTGGCTTGGTGGCGGCTTCAACAGAGCTGTTC	413				
DB	429 TTCTAGGTGAATTCGACAGATCAGAGATCAGACCTGGCTTGGTGGCGGCTTCAACAGAGCTGTTC	488				

QY		414	DATACCTTGCACGTCGTGGGTTTCAATTAAACCAATTATGGTGTAACAGCGGGTTGGCCA	473
Db		489	CATCACCTGCACAGACTCTCTGGTTCTTCTAATPACTAGCTATGGTGTAACTGGGGTTGCCCA	548
QY		474	GCCCTCAGGAAGAAGGCTGTGAGTGGCTGGAGTAGTAATGGGCTGGTGAAGCACAATA	533
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QY		534	TAAATTCGGCTCTTATGTCACAGCTGAGCATCAGACAGAACCACTCCAAAGGCCAAGTTTT	593
Db		609	TAAAGCAGCTTTCAATATCCAGACTGACATCAGACAAAGCAATTCCAAAGGCCAAGTTTT	668
QY		594	CTTAAAATGAAGACGTCGCAAACTGATGACACAGGCATGATACACTGTGCAGTGGGG	653
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QY		654	GGGTAACTACGCGCTATCTCTTGGACTACTGCGGGTCMAAGAACCTCACTCAACCTCTCC	711
Db		728	-----AGAACTGCGTCTTTTGGCTTACTGGGGCCAAAGGACCACGCTCACCGCTCTCC	777
RESULT 6				
LOCUS	AX023361	1389 bp	DNA	linear PAT 15-SEP-2000
DEFINITION	Sequence 32 from Patent WO0006605.			
ACCESSION	AX023361			
VERSION	AX023361.1	GI:10183773		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	Kufner,P., Zetcl,F., Dreier,T., Baeuerle,P.A. and Borschert,K.			
AUTHORS	1			
TITLE	Heteromimibodies			
JOURNAL	Patient: WO 0006605-A 32 10-FEB-2000;			
	KUERNER PERBER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;			
	BAEUEERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER			
	BIOMEDIZINIS (DE)			
FEATURES	location/Qualifiers			
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ORIGIN				
	Query Match 66.9%; Score 478; DB 6; Length 1389;			
	Best Local Similarity 81.5%; Pred. No. 4.8e-116;			
	Matches 585; Conservative 0; Mismatch 115; Indels 18; Gaps 2;			
QY		3	TATGTGTATGATCCAGACTCCCAAAATTCGCTGTATGACGAGGAGACAGGGTTACAT	62
Db		69	TATCACCTGACCCAGCTCTCAAAAATTCATGTCACATCAGTAGGAACAGGGTCAAGCT	128
QY		63	AACCTGGAAGCCACAGTGCAGAGTGTGAATATGATGTGGCTTGGTACCAAGAACCCAG	122
Db		129	CACCTGCAAGGCCACAGTGCAGATGTGGGTACTAATATGAGCCTGTGATTAACAGAAACCAG	188
QY		123	GCAGTCTCCGAACCTGCTGATATACTCTGCATCCAAATGCGTACACTGGAAGTCCCCTGATGC	182

Db 189 GCAATCTCTTAAGACATGATTTTACTCGGATCTTAACCGTACAGTGGAGTCCCTGATCG 248
Qy 183 CTTCACTGGCAGTGGATATGAGCAGGATTTTCACTTCACTCACTGACAGACTGTGACAGCTGA 242
Db 249 CTTCAACAGGAGTGGATCTGGACAGATTTTCACTCTCACTCACTGACAGATGTGAGCTGA 308
Qy 243 AGACCTGGCAGTATTTTCTGTCAAGCAGATTTAAGCT-----CGCTCGAAGGGGG 293
Db 309 AGACTGGCAGAGATTTTCTGTCAAGATATTAACAGCTATCCGCTCAAGTTGGTGTGG 368
Qy 294 GACCAAGCTGGAATTAAGAGTGGAGCGGTTCAAGCGGAGTGGCTTGGCGGGCGG 353
Db 369 GACCAAGCTGAGATCAAGAGTGGAGTGGTGTGTGTGGCGGCGGCGCTCGGTGGTGG 428
Qy 354 ATCCAGAGTGCAGGTGAAGAGTGAAGACAGCTGGCGTGGTGGCGCTTCAAGAGCTGTG 413
Db 429 TTCTCAGGTGAATGTGAGAGTCAAGACCTGGCTAGTGCAGGCCCTCAGAGAGCTGTG 488
Qy 414 CATCACTTGCACGTCTGTGGGTTTTCATTAAACCAATTATGTGTACACTGGGTTCCGA 473
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Qy 594 CTTAAATATGAACAGTCTGCAAACTGATGACACAGCCATGTACTACTGTGCAAGTGGG 653
Db 669 CTTAAATATGAACAGTCTGCAAACTGATGACACAGCCATATATTAATGTGCAAGTGG- 727
Qy 654 GGGTAACAGCGCTATGCTTGGACTATGAGTGGGTCAAGAACTTCAGTCAAGTCTCC 711
Db 728 -----AGAACTGTGCTGTTGCTTACTGGGGCCAAAGGACCAAGGTCACCGTCTCC 777

RESULT 7

LOCUS CO856167 1380 bp DNA linear PAT 31-AUG-2004
DEFINITION Sequence 19 from Patent WO2004069876.
ACCESSION CO856167
VERSION CO856167.1 GI:5185092
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Kischel,R., Kufner,P., Lutterbuese,R., Offner,S. and Wolf,A.
TITLE Enduring t cell response
JOURNAL Patent: WO 2004069876-A 19 19-AUG-2004;
MICROMET AG (DE)

FEATURES
Source Location/Qualifiers
1..1380

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="scfv antiBpCAM-hu4-1BBL nucleic acid sequence"

ORIGIN

Query Match 66.6%; Score 475.2; DB 6; Length 1380;
Best Local Similarity 81.1%; Pred. No. 2.7e-115;
Matches 584; Conservative 0; Mismatches 118; Indels 18; Gaps 2;
Qy 3 TATGTGATGACCCAGACTCCCAATTTCTGCTTATACAGACAGAGCAGGGTTACAT 62
Db 3 TATCCAGCTGACCCAGCTCTCCAAATTTATGTCCACATCAGTAGAGACAGGGTCAAGGT 62
Qy 63 AACCTGCAAGGCGAGTGCAGAGTGTAGTAATGATGTGGCTGTGTCCAAAGAACCCAGG 122

Db 63 CACCTGCAAGGCGAGTGCAGATGTGGTACTAATATGATGACCTGTGTATCAAGAAACCAGG 122
Qy 123 GCACTTCCGAACTGCTGATATATCTGCATTCATTCGCTACATGAGTCCCTGATCG 182
Db 123 GCAATCTCTTAAGACATGATTTTACTCGGATCTTACCTGAGTGGAGTCCCTGATCG 182
Qy 183 CTTCACTGGCAGTGGATATGAGCAGGATTTTCACTTCACTCACTGACAGACTGTGACAGCTGA 242
Db 183 CTTCAACAGGAGTGGATCTGGACAGATTTTCACTCTCACTCACTGACAGATGTGAGCTGA 242
Qy 243 AGACCTGGCAGTATTTTCTGTCAAGCAGATTTAAGCT-----CGCTCGAAGGGGG 293
Db 243 AGACTTGGCAGAGATTTTCTGTCAAGATATTAACAGCTATCCGCTCAAGTTGGTGG 302
Qy 294 GACCAAGCTGGAATTAAGAGTGGAGCGGTTCAAGCGGAGTGGCTTGGCGGGCGG 353
Db 303 GACCAAGCTGAGATCAAGAGTGGAGTGGTGTGTGTGGCGGCGGCTCGGTGGTGG 362
Qy 354 ATCCAGAGTGCAGGTGAAGAGTGAAGACAGCTGGCGTGGCGGCTTCAAGAGCTGTG 413
Db 363 TTCTCAGGTGAATGTGAGAGTCAAGACCTGGCTAGTGCAGGCCCTCAGAGAGCTGTG 422
Qy 414 CATCACTTGCACGTCTGTGGGTTTTCATTAAACCAATTATGTGTACACTGGGTTCCGA 473
Db 423 CATCACTGCACAGTCTGTGGTTTCTATTAACTAGCTATGTGTACACTGGGTTCCGA 482
Qy 474 GCTTCCAGAAAGGGTCTGAGTGGCTGGAGTAAATATGGGCTGGTGAAGACAAATTA 533
Db 483 GTTCCAGAAAGGGTCTGAGTGGCTGGAGTAAATATGGGCTGGTGAAGACAACTA 542
Qy 534 TAATTCGGCTCTTATGTCCAGACTGAGCAGTCAAGAGCAACTCCAAAGCAATTTT 593
Db 543 TAATGCAGCTTTCATATCAACATGAGCATCAGCAAGGCAATTCAAAGACCAAGTTT 602
Qy 594 CTTAAATATGAACAGTCTGCAAACTGATGACACAGCCATGTACTACTGTGCAAGTGGG 653
Db 603 CTTAAATATGAACAGTCTGCAAACTGATGACACAGCCATATATTAATGTGCAAGTGG- 661
Qy 654 GGGTAACAGCGCTATGCTTGGACTATGAGTGGGTCAAGAACTTCAGTCAAGTCTCC 713
Db 662 -----AGAACTGTGCTGTTGCTTACTGGGGCCAAAGGACCAAGGTCACCGTCTCC 713

RESULT 8

LOCUS MUSVKLI 738 bp DNA linear ROD 14-DEC-1995
DEFINITION Mus musculus (clone H11) Ig kappa light chain V region (Vk), Ig heavy chain V region (Vh), and single chain Fv gene.
ACCESSION L41689
VERSION L41689.1 GI:1119223
KEYWORDS
SOURCE
ORGANISM
Mus musculus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Suckling,C.J., Stimson,W.H., Proctor,G.R., Bence,L.H., Brooks,L., Khalaf,A.L. and Tedford,C.M.
TITLE Catalytic Antibodies - Designed and Accidental
JOURNAL J. Chem. Soc. Perkin Trans. 1 (22), 2777-2780 (1993)
COMMENT
ORIGINAL SOURCE TEXT: Mus musculus (strain NZB x BALB/c, sub-species musculus) (clone: H11) male adult splenocyte DNA. Single chain Fv constructed from an Igk1 antibody which has been shown to catalyze a Diels Alder cycloaddition reaction.

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Source Location/Qualifiers
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/mol_type="genomic DNA"
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/sub_species="musculus"
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/sex="male"
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346..390
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ORIGIN
Query Match      60.5%; Score 432; DB 10; Length 738;
Best Local Similarity 79.0%; Pred. No. 8.6e-104;
Matches 580; Conservative 0; Mismatches 115; Indels 39; Gaps 4;

QY 11 TGACCAAGCTCCCAATTCCTGTTATACAGACAGAGACAGGGTTACCAATCACTGCA 70
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Db 14 TGACCAAGCTCCATCATCTCTGGCTGTGCTCAGAGAGAAAGTCATATAGAGCTGTA 73
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QY 71 AGGCCAGTCAGATGT-----GAGTAATGATGTGGCTTGTTACCAAC 112
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Db 74 AGTCCAGTCAAAAGTGTATTATACAGTCAATAGAGAACTCTGGCCTGGTACAGC 133
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QY 113 AGAAGCAGGGGAGTCTCCGAACTGCTATATATCTGCATCCATCGCTACACTGGAG 172
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Db 134 AGAAACCAAGGAGCTCTCTAAGCTGTATCTACTAGGCAATCACTAGGGAATCTGGTG 193
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QY 173 TCCCTGATCGCTTCACTGGCAGTGAATAGGAGCGAATTTCACTTACCACTCAGACCTG 232
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Db 194 TCCCTGATCGCTTCAACAGCAGTGATCTGGACAGATTTTACTTACCATCAGACGTG 253
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QY 233 TGAGAGCTAAGACCTGGCAGTTATTTCTGTACAGAGAG---TTATAGTCTGCTGGAG 289
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Db 254 TACACCTGAAGCTGGGACGTTTATTAAGTATCATTAATCACTCTCCACACCTTGGAG 313
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QY 290 GGGGACCAAGCTGGAATATAA-----GGTGAAGCGGTTGAGCGGAGTGGCT 340
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Db 314 GGGGACCAAGCTGGAATATAAAGTGTGACGCGGTGGCGATCTGGTGGGAGTGGCT 373
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QY 341 CTGGCGGTGGCGGATGCGAGGTGACGTGAAGAGTCAAGACCTGCTGGTGGCCCT 400
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Db 374 CCGCGGTGGCGGTTCTTGAAGTGCAGACTTCAGAGATCAGGACCTGGCTGGTGGCCCT 433
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QY 401 CACAGAGCTGTCCATCACTGTCAGTCTCTGGGTTTCATTACCAATTATAGGTAC 460
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QY 461 ACTGGTGGCCAGCCTCCAGGAAAGGTCGTGAGTGGCTGGAGTAATATGAGCTGGTG 520
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QY 521 GAAGCAAAATTATTAATTCGCTCTTATGTCCAGACTGACATCAGCAAGACACTCCA 580
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QY 581 AGAGCCAAATTTCTTAAATATGAACAGTCTGAAACGTATATCAACAGCATCTACT 640
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Db 614 AGAGCCAAATTTCTTAAATATGAACAGTCTGAAACGTATATCAACAGCATCTACT 673
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QY 641 GTGCCAGTGGGGGGGTAACTACGAGCTATGCTTTGAGACTGAGGCTCAAGAACTCAG 700
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Db 674 GTGCCAGAGAGAGAGAT-----TATAGCTTACTACTGTGGGCCAAGGACACAGG 724
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QY 701 TCACGCTCTCTCA 714
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Db 725 TCACGCTCTGATCA 738
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RESULT 9
MM295476      840 bp      mRNA      linear      ROD 29-OCT-1997
LOCUS        MM295476
DEFINITION   Mus musculus mRNA for Igm/kappa antibody, sefvGUS-CK.
ACCESSION   Z95476 AF004403
VERSION     Z95476.1 GI:2108308
KEYWORDS     IGM.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 840)
AUTHORS      Schouten,A., Roostien,J., de Boer,J.M., Wilmlink,A., Rosso,M.N.,
              Bosch,D., Stiekema,W.J., Gommers,F.J., Bakker,U. and Schots,A.
              Improving scFv antibody expression levels in the plant cytosol
              FEBS Lett. 415 (2), 235-241 (1997)
JOURNAL      MEDLINE 98010486
PUBMED      9351003
REFERENCE    2 (bases 1 to 840)
              Schouten,A.
              Direct Submision
              Submitted (07-MAY-1997) Dept. of Nematology, Wageningen
              Agricultural University, P.O. Box 8123, Wageningen 6700 BS, The
              Netherlands
FEATURES
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/protein_id="CAB08854.1"

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misc_feature
826..837
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ORIGIN

Query Match 58.4%; Score 417.2; DB 10; Length 840;
Best Local Similarity 76.3%; Pred. No. 7.3e-100;
Matches 563; Conservative 0; Mismatches 148; Indels 27; Gaps 3;
QY 4 ATTGTGATGACCCGAGCTCCCAATTCCTGCTGTATACAGAGAGAGAGGTTACCTA 63
DB 22 ATTCAGATGACACAGTCTCCCACTCTGCTGTGTGAGAGAGAGAGGTCATATG 81
QY 64 AACTGCAAGGCGAGTCAGAGTGT-----GAGTAATGATGTGGCTTGG 105
DB 82 AGCTGTAAGTCAAGTCAAAAGTGTTTATACAGTTCAATCAGAGAACTAATTGGCC 141
QY 106 TACCAACAGAGACCAAGGCGAGTCTCCGAACTGCTGATATACCTGATCAATGCTAC 165
DB 142 TACCAAGAGAAACAGAGGCGAGTCTCTTAACCTGATCTAGTGGCTTCCACTAGGAA 201
QY 166 ACTGAGTCCCTGATCGCTTACCTGAGTGAATGAGAGAGAGATTTACCTTACCATC 225
DB 202 TCCGATGCTCTGATGCTTACAGAGGAGTGAATCTGGAGACAGATTTTACCTTACCATC 261
QY 226 AGCAGTGCAGAGCTGAAAGCTGCGAGTATTTCTGTACAGAGATTAATAGCTGC-- 283
DB 262 AGCAGTGCAGAGCTGAAAGCTGCGAGTATTTCTGTACATCAATCACTCTCTGCTGC 321
QY 284 ----TCGAGAGGGGAGCCAAAGCTGGAATAAAGGTGAGCGGTTCAAGCGAGAGTGGC 339
DB 322 ACCTTCGATGCGGGGAGCCAAAGCTGGAATAAAGCGAGGGTAAATCTCTCAGAGATCTGC 381
QY 340 TCTG---CGGATGCGGATTCGAGGTGAGGTGAAGAGTCAAGACCTGCGCTGTGGCG 396
DB 382 TCCCAATTCCAAACTGAGTCTGAGGTGAACCTGAGTGAATCTGAGCCTGAGCTGTAG 441
QY 397 CCGTCACAGAGCTGTGCATCACTTGCAGTGTCTGTGGTTTTCATTAACCAATTAATG 456
DB 442 CCTCAAGAGCTGTGCATCACTTGCAGTGTCTGTGGTTTTCATTAACCAATTAATG 501
QY 457 GTACACTGGGTTTGCAGAGCTTCAAGAAAGGATCTGAGTGGCTGAGAGTAAATGAGCT 516
DB 502 GTACACTGGGTTTGCAGAGCTTCAAGAAAGGATCTGAGTGGCTGAGAGTAAATGAGGA 561
QY 517 GGTGAAGACAAATTAATTCGGCTTTATGTCAGACTGAGCATAGCAAGACCAAC 576
DB 562 GGTGAAGACAAAGTCAATGACAGCTTCAATGTCAGACTGAGCATAGCAAGACCAAC 621
QY 577 TCCAAGAGCAAGTTTCTTAATAATGAACAGTCTGCAACATGATGACAGAGCCATGAC 636
DB 622 TCCAAGAGCAAGTTTCTTAATAATGAACAGTCTGCAAGCTGATGACAGAGCCATGAC 681
QY 637 TACTGTGCAAGTCCGGGGGATTAATGAGGCTATGCTTTGATGATGAGGATCAAGAAC 696
DB 682 TACTGTGCAAAATTAATGATGATTAATGAGGCTATGATGAGGATCAAGAAC 741

QY 697 TCAGTCAAGCTCTCTCA 714
DB 742 TCAGTCAAGCTCTCTCA 759

RESULT 10
AR481833
LOCUS AR481833 752 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 31 from patent US 6699715.
ACCESSION AR481833
VERSION AR481833.1 GI:47243499
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 752)
AUTHORS Ledbetter,J.A., Hayden,M., Fell,P., Mitterler,R. and Winberg,G.
TITLE Modified sfv molecules which mediate adhesion between cells and
uses thereof
JOURNAL Patent: US 6699715-A 31 02-MAR-2004;
FEATURES
LOCATION/Qualifiers
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ORIGIN

Query Match 58.0%; Score 414.4; DB 6; Length 752;
Best Local Similarity 76.9%; Pred. No. 4.1e-99;
Matches 569; Conservative 0; Mismatches 141; Indels 30; Gaps 4;
QY 4 ATTGTGATGACCCGAGCTCCCAATTCCTGCTGTATACAGAGAGAGAGGTTACCTA 63
DB 7 ATTGTGCTACCCATCTCCAGCTTCTTGCTGTGTCTAGTCAAGAGCCACCATC 66
QY 64 AACTGCAAGGCGAGTCAGAGTGTGATGATGATGCT-----TGTACAA 111
DB 67 TCTGAGAGAGCAGTGAAGTGAATATTAATGTCAGAGTTAATGAGAGTGTACAA 126
QY 112 CAGAGCCAGGAGCTCTCCGAACTGCTGATATCTGTGATCAATTCGATCACTGGA 171
DB 127 CAGAAACAGAGACGAGCCAACTCTCATCTCTGATCACTCAAGTAACTTGGG 186
QY 172 GTCCCTGATGCTTCACTGAGAGTGAATGAGAGAGATTTCACTTACCATCAGACT 231
DB 187 GTCCCTCAGAGTTAGTGAAGTGTGAGGACACTTCACTTCAATCATCTT 246
QY 232 GTGAGGCTGAGAGCTGAGAGTATTTCTGTGAG-----AGATTATAGCTCG 282
DB 247 GTGAGAGAGATGATATTTGCAATGATATTTCTGTGAGAGAGTGAAGGTTCTTGAAG 306
QY 283 CTCGAGAGGGGAGCAAGCTGGAATTA---GTGAGAGCGGTTTCAAGCGAGTGGC 339
DB 307 TTCGATGAGAGCAAGAGCTGGAATTAAGAGGAGTGGCTGCGGCGGTGTGGG 366
QY 340 TCTGCGGCTGCGGATTCGAGTCAAGTGAAGAGTCAAGAGCTGAGCTGTGGTGGCC 399
DB 367 TCGGATGCGGCGGATTCGAGTCAAGTGAAGAGTCAAGAGCTGAGCTGTGGTGGCC 426
QY 400 TCACAGAGCTGTGCATCACTTGCAGTGTCTGTGGTTTTCATTAACCAATTAATGATG 459
DB 427 TCACAGAGCTGTGCATCACTTGCAGTGTCTGTGGTTTTCATTAACCGGATATGATG 486
QY 460 CACTGAGTGGCCAGCTTCAAGAAAGGATGAGTGGCTGAGAGTAAATGAGGCTGT 519
DB 487 AACTGAGTGGCCAGCTTCAAGAAAGGATGAGTGGCTGAGAGTAAATGAGGCTGT 546
QY 520 GGAAGCAAAATTAATTCGGCTTTATGTCAGACTGAGCATAGCAAGACCAATGCC 579
DB 547 GGAAGCAAAATTAATTCAGCTTCAATTCAGACTGAGCATAGCAAGACCAATGCC 606
QY 580 AAGAGCAAGTTTCTTAATAATGAACAGTCTGCAACATGATGACAGGCAATGATAC 639

Db 607 AAGAGCCAAAGTTTCTTAAATGAACAGTCTGCAAACTGATGACACAGCCAGACTACTAC 666
Qy 640 TGTGCCAGTGGGGGGGTAAGTACTAC-----GGCTATGCTTTGGACCTACTAGGGGTCAAGA 693
Db 667 TGTGCCAGAGATGTTATAGTAAGTCTTCACTATGTTATGACACTCTGGGGTCAAGA 726
Qy 694 ACCTCACTACCGTCTCTC 713
Db 727 ACCTCACTACCGTCTCTC 746

RESULT 11
AR481832
LOCUS AR481832 1509 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 30 from patent US 669715.
ACCESSION AR481832
VERSION AR481832.1 GI:47243498
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1509)
AUTHORS Ledbetter,J.A., Hayden,M., Fell,P., Mittler,R. and Winberg,G.
TITLE Modified svf molecules which mediate adhesion between cells and
uses thereof
JOURNAL Patent: US 669715-A 30 02-MAR-2004;
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 58.0%; Score 414.4; DB 6; Length 1509;
Best Local Similarity 76.9%; Pred. No. 3.9e-99;
Matches 569; Conservative 0; Mismatches 141; Indels 30; Gaps 4;

Qy 4 ATTGTGATGACCCAGACTCCCAATTCCTGCTGTATCAGCAGAGACAGGGTTACCAT 63
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Qy 64 ACCTGCAAGCCAGTCAAGTGTGATGATGTGGCT-----TGGTACCA 111
Db 61 TCTGCGAGACCAAGTGAAGTGTGAATATGTCACAAAGTTTAATGACAGTGTACCA 120
Qy 112 CAGAGCCAGGGAGTCTCGAAACTGCTGATATACCTGCAATCCCAATGCTACCTGA 171
Db 121 CAGAAACAGAGACAGCCACCAATCTCTCATCTGCTGATCCAGTGAATCTGGG 180
Qy 172 GTCCCTGATCGCTTCACTGCAAGTGAATGAGACGAGATTTCACCTACAGCACT 231
Db 181 GTCCCTGCAAGTTTATGAGAGTGGGTCTGGGACAGACTTCAGCCCTCAACATCCATCCT 240
Qy 232 GTGCAAGCTGAAGACTGCGAGTTTATTTCTGTACG-----AGATTAATAGCTG 282
Db 241 GTGAGAGAGATGATATGCAATGTATTTCTGTACAGAAAGTAGAAGTTCCTTGGACG 300
Qy 283 CTGGAAGGGGGGACCAAGCTGGAATAA---GTTGAGAGCGGTTCAAGCGAGGTGGC 339
Db 301 TTGCTGTGAAGACCAAGCTGGAATCAAAAGGGGTGGCTGGCGGGGTGGG 360
Qy 340 TCTGGCGGTGGCGGATGCGAGTGCAGTGAAGAGTCAAGACCTGAGCTGTGGCGCC 399
Db 361 TCGGGTGGCGCGGATCTCAGTGCAGTGAAGAGTCAAGACCTGAGCTGTGGCGCC 420
Qy 400 TCACAGAGCTGTTCATCACTTGTGCACTGTCTGTGGTTTCAATTAACCAATTAATGATGA 459
Db 421 TCACAGAGCTGTTCATCACTTGTGCACTGTCTGTGGTTTCAATTAACCGGCTATGATGA 480
Qy 460 CACTGGTTTGGCAAGCTTCAAGAAAGAGTCTGAGTGGCTGGGAGTAATATGGGCTGT 519
Db 481 AACTGGTGGCGGCTTCAAGAAAGAGTCTGAGTGGCTGGGAGTAATATGGGCTGT 540
Qy 520 GGAAGCAAAATTAATATGCGCTTATGTCAGACTGAGCATCAGCAAGAACCACTCC 579

Db 541 GGAAGCAGACTATATATTCAGCTTCAATCAGCTGAGATCCAGAGACCACTCC 600
Qy 580 AAGAGCCAGTTTCTTAAATGAACAGTCTGCAAACTGATGACACAGCCAGTACTAC 639
Db 601 AAGAGCCAAAGTTTCTTAAATGAACAGTCTGCAAACTGATGACACAGCCAGTACTAC 660
Qy 640 TGTGCCAGTGGGGGGGTAAGTACTAC-----GGCTATGCTTTGGACCTACTAGGGGTCAAGA 693
Db 661 TGTGCCAGAGATGTTATAGTAAGTCTTCACTATGTTATGACACTCTGGGGTCAAGA 720
Qy 694 ACCTCACTACCGTCTCTC 713
Db 721 ACCTCACTACCGTCTCTC 740

RESULT 12
AR481831
LOCUS AR481831 1527 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 29 from patent US 669715.
ACCESSION AR481831
VERSION AR481831.1 GI:47243497
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1527)
AUTHORS Ledbetter,J.A., Hayden,M., Fell,P., Mittler,R. and Winberg,G.
TITLE Modified svf molecules which mediate adhesion between cells and
uses thereof
JOURNAL Patent: US 669715-A 29 02-MAR-2004;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 58.0%; Score 414.4; DB 6; Length 1527;
Best Local Similarity 76.9%; Pred. No. 3.9e-99;
Matches 569; Conservative 0; Mismatches 141; Indels 30; Gaps 4;

Qy 4 ATTGTGATGACCCAGACTCCCAATTCCTGCTGTATCAGCAGAGACAGGGTTACCAT 63
Db 1 ATTGTGCTACCCCAATCTCAGCTTCTTGGCTGTCTCTAGGTGACAGACCATC 60
Qy 64 ACCTGCAAGCCAGTCAAGTGTGATGATGTGGCT-----TGGTACCA 111
Db 61 TCTGCGAGACCAAGTGAAGTGTGAATATGTCACAAAGTTTAATGACAGTGTACCA 120
Qy 112 CAGAAACAGAGACAGCCACCAATCTCTCATCTGCTGATCCAGTGAATCTGGG 180
Db 121 CAGAAACAGAGACAGCCACCAATCTCTCATCTGCTGATCCAGTGAATCTGGG 180
Qy 172 GTCCCTGATCGCTTCACTGCAAGTGAATGAGACGAGATTTCACCTACAGCACT 231
Db 181 GTCCCTGCAAGTTTATGAGAGTGGGTCTGGGACAGACTTCAGCCCTCAACATCCATCCT 240
Qy 232 GTGCAAGCTGAAGACTGCGAGTTTATTTCTGTACG-----AGATTAATAGCTG 282
Db 241 GTGAGAGAGATGATATGCAATGTATTTCTGTACAGAAAGTAGAAGGTTCTTGGACG 300
Qy 283 CTGGAAGGGGGGACCAAGCTGGAATAA---GTTGAGAGCGGTTCAAGCGAGGTGGC 339
Db 301 TTGCTGTGAAGACCAAGCTGGAATCAAAAGGGGTGGCTGGCGGGGTGGG 360
Qy 340 TCTGGCGGTGGCGGATGCGAGTGCAGTGAAGAGTCAAGACCTGAGCTGTGGCGCC 399
Db 361 TCGGGTGGCGCGGATCTCAGTGCAGTGAAGAGTCAAGACCTGAGCTGTGGCGCC 420
Qy 400 TCACAGAGCTGTTCATCACTTGTGCACTGTCTGTGGTTTCAATTAACCAATTAATGATGA 459
Db 421 TCACAGAGCTGTTCATCACTTGTGCACTGTCTGTGGTTTCAATTAACCGGCTATGATGA 480

Qy 460 CACTGGGTTCCGACGCTCCAGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCTGGT 519
Db 481 AACTGGGTTCCGACGCTCCAGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCTGGT 540
Qy 520 GGAAGCAAAATTAATTCGGCTTTATGTCAGACTGAGCAATGAGCAAGCAATTC 579
Db 541 GGAAGCAAGACTTAATTCAGCTCTCAATTCAGACTGAGCAATGAGCAAGCAATTC 600
Qy 580 AAGAGCAAGTTTCTTAATAAATGAACAGTCTGAAATGATGACACAGCCATGACTAC 639
Db 601 AAGAGCAAGTTTCTTAATAAATGAACAGTCTGAAATGATGACACAGCCATGACTAC 660
Qy 640 TGTCCAGAGTGGGGGGGTAAGTAC-----GGCTATGCTTGGACTACTGGGGTCAAGGA 693
Db 661 TGTCCAGAGTGGTATATGTAATCTTCTATCTATCTATGATGACTACTGGGGTCAAGGA 720
Qy 694 ACCTGAGTACCGTCTCTC 713
Db 721 ACCTGAGTACCGTCTCTC 740

RESULT 13

AR364987 729 bp DNA linear PAT 03-SEP-2003
LOCUS AR364987
DEFINITION Sequence 16 from patent US 5455030.
ACCESSION AR364987
VERSION AR364987.1 GI:34428209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 729)
Unclasseified.

REFERENCE
AUTHORS Ladner,R.C., Bird,R.E. and Hardman,K.
TITLE Immunotherapy using single chain polypeptide binding molecules
JOURNAL Patent: US 5455030-A 16 03-OCT-1995;
FEATURES
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ORIGIN

Query Match 57.2%; Score 408.2; DB 6; Length 729;
Best Local Similarity 75.8%; Pred. No. 1.8e-97;
Matches 548; Conservative 0; Mismatches 163; Indels 12; Gaps 3;
Qy 4 ATTGTGATGACCCAGACTCCCAATTCCTGCTTGTATCAGAGAGAGACAGGTTACCATTA 63
Db 7 AATGTGCTCACCCAGCTCTCCAGCAATCATGTCTGCATCTCCAGGGGAAAGTCAACCATG 66
Qy 64 ACCTGCAAGGCGCACTCAGAGTGTAGT---AATGATGTGCTTGGTATCCACAGAAAGCA 120
Db 67 ACCGCAAGGGCGCACTCAGAGTGTAGT---AATGATGTGCTTGGTATCCACAGAAAGCA 126
Qy 121 GGGGAGTCTCCGAAGTGTATATCTGTCATCCAAATGCTACAGTGGAGTCCCTGAT 180
Db 127 GGTCCCTCCCAAACTCTGGGTTTATGACATCCAACTTGGCTTCTGGAGTCCCTGAT 186
Qy 181 CGCTTCACTGGCAGTATATGAGACGAGATTTCATTTACACATCAGACATGTCAGGCT 240
Db 187 CGCTTCACTGGCAGTATATGAGACGAGATTTCATTTACACATCAGACATGTCAGGCT 246
Qy 241 GAAGACCTGGCAGTTTATTTCTGTCAGAG-----GATTATAGTCTGCTGGAGGGGG 294
Db 247 GAAGATCTGGCAGTTTATTTCTGTCAGAG-----GATTATAGTCTGCTGGAGGGGG 306
Qy 295 ACCAAGCTGGAATTAAGAGTGAAGCGGTTCAAGCGGAGGTGCTGGCGGTGGCGGA 354
Db 307 CCCACCAAGCTTAAGAGTGAAGCGGTTCTGTTCTTCTTAACACGCTGGCTCAATTCCT 366
Qy 355 TCGCAGGTGACAGTGAAGAGTCAAGACCTGGCTGGTGGCGCCCTCAAGAGCCTGTC 414
Db 367 CTGATGTGACAGTGAAGAGTCAAGACCTGCTGGTGGCGCCCTCAAGAGCCTGTC 426

Qy 415 ATCACTTGCACTGTCTCTGGGTTTTCATTAACCAATTATGTTGACACTGGGTTCCGAC 474
Db 427 ATCACTTGCACTGTCTCTGGGTTTTCATTAACCAATTATGTTGACACTGGGTTCCGAC 486
Qy 475 CTTCCAGAAAGGTTCTGGAGTGGCTGGAGTAATATGGGCTGGTGAAGCAAAATTAT 534
Db 487 CTTCCAGAAAGGTTCTGGAGTGGCTGGAGTAATATGGGCTGGTGAAGCAAAATTAT 546
Qy 535 AATTGGCTCTTAATGTCAGATGAGATCAGACAGCAAGCAATTCAGAGCAAGTTTC 594
Db 547 AATTGACCTCTCAATGTCAGATGAGATCAGACAGCAATTCAGAGCAAGTTTC 606
Qy 595 TTAATAATGAACAGTCTGCAAACTGATGACAGCCATGTAAGTCTGTCGCA---GTCCG 651
Db 607 TTAATAATGAACAGTCTGCAAACTGATGACAGCCATGTAAGTCTGTCGCAAACTG 666
Qy 652 GGGGTAAGTACGAGCTATGCTTTGGACTACTGGGGTCAAGAACTGACCGTCTCC 711
Db 667 GAACGAATCTTTACTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 726
Qy 712 TCA 714
Db 727 TAA 729

RESULT 14

SYN507107 1632 bp RNA linear SYN 02-SEP-2002
LOCUS SYN507107
DEFINITION Synthetic construct for anti-CD28 and anti-HMWG scFv antibody,
clone r28M.
ACCESSION AJ507107
VERSION AJ507107.1 GI:22759563
KEYWORDS antibody; heavy chain; immunoglobulin; light chain; scFv; variable region.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE
AUTHORS Grosse-Hovest,L.
TITLE Produktion und Charakterisierung supra-agonistischer bipezifischer CD28-Antikörper zur Tumor-Immuntherapie
JOURNAL Thesis (2002) Department of Biology, University of Tuebingen, Tuebingen, Germany
REFERENCE
AUTHORS Grosse-Hovest,L.
TITLE Direct Submission
JOURNAL Submitted (28-AUG-2002) Grosse-Hovest L., Membrane Biochemistry, Max-Planck-Institute for Biochemistry, Am Klopferspitz 18a, 82152 Martinsried, GERMANY

FEATURES

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/mol_type="other RNA"
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856. 1218
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source

CDS

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NSKSOYFLIKNSLQADDTAVYCARDKGYSVYVSMYMGCTTVYSSASTKPSVP
LAPSSSGGVKLOQSGPELVKPGASYKISCKASGAFSSMMNWKORQGLMENG
RIYPGSDINYNKRFKPKATLVADKSSSTAVMVOSSLTVSDAVYFCARGNTVVPYT
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1264..1599
/product="immunoglobulin light chain variable region"

ORIGIN

Query Match 57.1%; Score 407.8; DB 12; Length 1632;
Best Local Similarity 76.4%; Pred. No. 2.2e-97;
Matches 563; Conservative 0; Mismatches 147; Indels 27; Gaps 4;

QY 4 ATTGTGATGACCAAGTCTCCAAATTCCTGTTGATCAGAGAGAGAGGTTTACCATA 63
DB 61 ATGAGGTCACACTAGTCTCAGCTCTTGGCTGTGCTCTAAGGCAGAGACCATC 120
QY 64 ACCTGCAAGGCCAGTCAAGTGTGAATGATGTCAGAGTTAATGACAGTGTACAG 180
DB 121 TCCTGCAAGGCCAGTCAAGTGTGAATGATGTCAGAGTTAATGACAGTGTACAG 180
QY 112 CAGAAAGCCAGGAGCTCTCGAAATCTGATATACCTGATCCAAATGCTACACTGA 171
DB 181 CAGAAAGCCAGGAGCTCTCGAAATCTGATATACCTGATCCAAATGCTACACTGA 240
QY 172 GTCCCTGATGCTTCACTGGCAGTGAATGGAACGATTTCACTTTCACATCAGACT 231
DB 241 GTCCCTGAGGTTTGTAGTGGCAGTGGGTCTGGGACAAATCTTCAAGCTCAATCCATCCT 300
QY 232 GTCCAGGCTGAACCTCGCAGTTTATTTCTGTACG-----AGATTATAGCTG 282
DB 301 GTGAGAGAGATATGTTGCAATGTAATTTCTGTACAGAAAGTAGAAGGTTCTTACAG 360
QY 283 CTCGAGAGGGGAGCAAGCTGGAATTAATAA---GGTGAAGCGGTTCAAGGCGAGGTGCG 339
DB 361 TTTCGAGAGGGGAGCAAGCTGGAATTAATAAAGGAGGCGCGGTTCTGGCGGTGGCGGA 420
QY 340 TCTGGCGGTGGCGGATTCGAGGTGCAAGTGAAGAGTCAAGACCTGGCTGTGGCGGCC 399
DB 421 TCAGGTGGCGGAGCTTCGAGGTGAATCTGACAGAGTCTGGCTGTGGCGGCC 480
QY 400 TCACAGAGCTGTTCATCACTTGTGCACTGTCTGGGTTTCAATTAACCAATTATGCTGA 459
DB 481 TCACAGAGCTGTTCATCACTTGTGCACTGTCTGGGTTTCAATTAACCAATTATGCTGA 540

QY 460 CACTGGGTTTCGACGAGCTCCAGAAAGGCTGTGAGTGGCTGGAGTAATATGCGTGT 519
DB 541 CACTGGGTTTCGACGAGCTCCAGAGACAGGAGCTGAGATGGTGGAGATTAATATGGGCTGT 600
QY 520 GGAAGCACAATTAATTAATTTGGCTTTATGTCACACTGACATCAGCAAGCAACTCC 579
DB 601 GGAGGACAGCAATTAATTAATTTGGCTTCATGTCAGAAAGGCAATCAGCAACTCC 660
QY 580 AAGAGCAAGTTTCTTAATAAATGAACAGTCTGCAACTGATGACACAGCCATGTACTAC 639
DB 661 AAGAGCAAGTTTCTTAATAAATGAACAGTCTGCAACTGATGACACAGCCATGTACTAC 720
QY 640 TGTGCCAG--TCGGGCGGTTAACTACGAGCTATGCTTTGGACTTACCTGAGGCTCAAGAAC 696
DB 721 TGTGCCAGATTAAGGATTAATCTCTATTACTATTATGAGACTACGAGGCGCAAGGAGCC 780
QY 697 TCAGTCAACGCTCTCTC 713
DB 781 ACGGTCACTGTCTCTC 797

RESULT 15

AR481837 824 bp DNA linear PAT 14-MAY-2004
LOCUS AR481837
DEFINITION Sequence 38 from patent US 6699715.
ACCESSION AR481837
VERSION AR481837.1 GI:47243503
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 824)
AUTHORS Ledbetter J.A., Hayden M., Fell P., Mittleer R. and Winberg G.
TITLE Modified sFv molecules which mediate adhesion between cells and
uses thereof
JOURNAL Patent: US 6699715-A 38 02-MAR-2004;
FEATURES Location/Qualifiers
source 1..824
/organism="unknown"
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ORIGIN

Query Match 56.1%; Score 400.2; DB 6; Length 824;
Best Local Similarity 76.4%; Pred. No. 2.4e-95;
Matches 572; Conservative 0; Mismatches 138; Indels 39; Gaps 5;

QY 4 ATTGTGATGACCAAGTCTCCAAATTCCTGTTGATCAGAGAGAGAGGTTTACCATA 63
DB 70 ATTGTGCTACCAACCAATCTCAGCTCTTGGCTGTGCTCTTGAAGGCGAGAGCCACCATC 129
QY 64 ACCTGCAAGGCCAGTCAAGTGTGAATGATGTCAGAGTTAATGACAGTGTACAG 180
DB 130 TCCTGCAAGGCCAGTCAAGTGTGAATGATGTCAGAGTTAATGACAGTGTACAG 189
QY 112 CAGAAAGCCAGGAGCTCTCGAAATCTGATATACCTGATCCAAATGCTACACTGA 171
DB 190 CAGAAAGCCAGGAGCTCTCGAAATCTGATATACCTGATCCAAATGCTACACTGA 249
QY 172 GTCCCTGATGCTTCACTGGCAGTGAATGGAACGATTTCACTTTCACATCAGACT 231
DB 250 GTCCCTGAGGTTTGTAGTGGCAGTGGGTCTGGGACAAATCTTCAAGCTCAATCCATCCT 309
QY 232 GTCCAGGCTGAACCTCGCAGTTTATTTCTGTACG-----AGATTATAGCTG 282
DB 310 GTGAGAGAGATATGTTGCAATGTAATTTCTGTACAGAAAGTAGAAGGTTCTTACAG 369
QY 283 CTCGAGAGGGGAGCAAGCTGGAATTAATAA---GGTGAAGCGGTTCAAGGCGAGGTGCG 333
DB 370 TTTCGAGAGGGGAGCAAGCTGGAATTAATAAAGGAGGCGCGGTTCTGGCGGTGGCGGA 429
QY 334 GGTGCTTGGCGGTGGCGGATTCG-----CAGTGCAGGTGAAGAGTCAAGACCTGGC 387
DB 430 GGTGCTTGGCGGTGGCGGATTCG-----CAGTGCAGGTGAAGAGTCAAGACCTGGC 489

CC soft tissue sarcomas, medulloblastomas, high grade astrocytomas,


```
Oy 301 CTGGAATATTAAGGTGAGGCGGTTTCAGAGCGGAGTGGCTCTGGCGGTGGCGGATTCGCAG 360
Db 301 CTGGAATATTAAGGTGAGGCGGTTTCAGAGCGGAGTGGCTCTGGCGGTGGCGGATTCGCAG 360
Oy 361 GTGCAAGGTGAAGAGTCAAGACCTGGCTGGTGGCGCCCTCAAGAGCCTGTCCATCACT 420
Db 361 GTGCAAGGTGAAGAGTCAAGACCTGGCTGGTGGCGCCCTCAAGAGCCTGTCCATCACT 420
Oy 421 TGCACTGTCTGGGTTTTCATTAAACCAATTATGTGTATCACTGGGTTCCGCACTCCA 480
Db 421 TGCACTGTCTGGGTTTTCATTAAACCAATTATGTGTATCACTGGGTTCCGCACTCCA 480
Oy 481 GGAAGGCTGTGAGTGGCTGGGATATATGGGCTGGTGAAGACAATTATTAATTCG 540
Db 481 GGAAGGCTGTGAGTGGCTGGGATATATGGGCTGGTGAAGACAATTATTAATTCG 540
Oy 541 GCTCTTATGTCCAGACTGAGCATCAAGAGCAACATCCAAAGCCAAAGTTTCTTAA 600
Db 541 GCTCTTATGTCCAGACTGAGCATCAAGAGCAACATCCAAAGCCAAAGTTTCTTAA 600
Oy 601 ATGAACAGTCTGCAAACTGATGACACAGCCATGTACTCTGCCAGTCCGGGGGTAA 660
Db 601 ATGAACAGTCTGCAAACTGATGACACAGCCATGTACTCTGCCAGTCCGGGGGTAA 660
Oy 661 TAGCGCTATGCTTTGGACTACTGGGGTCAAGAACTGACACCGTCTCTCA 714
Db 661 TAGCGCTATGCTTTGGACTACTGGGGTCAAGAACTGACACCGTCTCTCA 714

RESULT 3
AAT86312
ID AAT86312 standard; DNA; 1173 BP.
XX
AC AAT86312;
XX
DT 06-APR-1998 (first entry)
XX
DE Single chain anti-disialoganglioside GD2 antibody 3G6-scFv-streptavidin.
XX
KM Antibody construct; disialoganglioside; GD2; single chain Fv fragment;
KM scFv; tumour; neuroblastoma; osteosarcoma; soft tissue Sarcoma;
KM tissue imaging; target delivery; toxin; streptavidin;
KM pro-drug converting enzyme; GD2-targeted lymphocyte; ss.
XX
OS Synthetic.
XX
FH Key location/Qualifiers
FT misc_feature 1..714
FT /tag= a
FT /note= "encodes single chain Fv fragment of antibody 3G6"
FT misc_feature 715..738
FT /tag= b
FT /note= "linker sequence"
FT misc_feature 739
FT /tag= c
FT /note= "encodes streptavidin"
XX
XX WO9734634-A1.
XX
XX 25-SEP-1997.
XX
XX 20-MAR-1997; 97WO-US004427.
XX
XX 20-MAR-1997; 97WO-US004427.
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XX 20-MAR-1996; 96US-0013703P.
XX
XX (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
XX Cheung NV, Larson SM, Guo H, Rivlin K, Sadelain M;
XX
XX WPI; 1997-473996/44.
XX
XX Recombinant single chain anti-disialoganglioside GD2 antibody - useful to
XX detect tumour cells expressing GD2 and to target therapeutic agents, e.g.
XX
```

```
PT toxins, to such cells.
XX
XX Disclosure; Page 13; 31pp; English.
XX
XX The present sequence encodes a recombinant single chain peptide, 3G6-scFv
CC -streptavidin. The peptide is an antibody construct comprising the
CC variable regions of the heavy and light chains of an antibody against
CC disialoganglioside (GD2) as a single chain Fv fragment (scFv). GD2 occurs
CC in many tumours types including neuroblastoma, osteosarcomas and other
CC soft tissue sarcomas, medulloblastomas, high grade astrocytomas,
CC melanomas and small cell lung cancer. The peptide can be detectably
CC labelled, preferably with 99m-Tc, for tissue imaging of cells expressing
CC GD2. It can also be used to target delivery of a therapeutic or pre-
CC therapeutic agent, such as a toxin, streptavidin (e.g. present sequence)
CC or a pro-drug converting enzyme, to cells expressing GD2. The peptide may
CC further comprise CD8 to facilitate the formation of GD2-targeted
CC lymphocytes. T cells containing the peptide can also be used to target
CC GD2-producing tumour cells
XX
XX Sequence 1173 BP; 270 A; 334 C; 340 G; 229 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 714; DB 2; Length 1173;
XX Best Local Similarity 100.0%; Pred. No. 8.1e-198;
XX Matches 714; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AGTATTGTGATGACCCAGATCTCCCAATTCTCTGTGTATACAGAGAGACAGGTTTACC 60
Db 1 AGTATTGTGATGACCCAGATCTCCCAATTCTCTGTGTATACAGAGAGACAGGTTTACC 60
Oy 61 ATAACTGCAAGGCGCATGACAGAGTGTGATGATGATGCTGGTGTACCAAGAGCA 120
Db 61 ATAACTGCAAGGCGCATGACAGAGTGTGATGATGATGCTGGTGTACCAAGAGCA 120
Oy 121 GGGCAGTCTCCGAACCTGTGATATTAATCTGTGATCAATGCTACAGTGCCTGAT 180
Db 121 GGGCAGTCTCCGAACCTGTGATATTAATCTGTGATCAATGCTACAGTGCCTGAT 180
Oy 181 CGCTTCACTGGCAGTGTATGAGACCGGATTTTCACTTTCACACACACACTGTCCAGCT 240
Db 181 CGCTTCACTGGCAGTGTATGAGACCGGATTTTCACTTTCACACACACACTGTCCAGCT 240
Oy 241 GAAGACCTGGAGTTTATTTCTGTGACAGAGATTAATGCTGCTCGGAGGGGGACCAAG 300
Db 241 GAAGACCTGGAGTTTATTTCTGTGACAGAGATTAATGCTGCTCGGAGGGGGACCAAG 300
Oy 301 CTGGAATATTAAGGTGAGGCGGTTTCAGGCGAGGTGCTCTGGCGGTGGCGGATTCGCAG 360
Db 301 CTGGAATATTAAGGTGAGGCGGTTTCAGGCGAGGTGCTCTGGCGGTGGCGGATTCGCAG 360
Oy 361 GTGCAAGGTGAAGAGTCAAGACCTGGCTGGTGGCGCCCTCAAGAGCCTGTCCATCACT 420
Db 361 GTGCAAGGTGAAGAGTCAAGACCTGGCTGGTGGCGCCCTCAAGAGCCTGTCCATCACT 420
Oy 421 TGCACTGTCTGGGTTTTCATTAAACCAATTATGTGTATCACTGGGTTCCGCACTCCA 480
Db 421 TGCACTGTCTGGGTTTTCATTAAACCAATTATGTGTATCACTGGGTTCCGCACTCCA 480
Oy 481 GGAAGGCTGTGAGTGGCTGGGATATATGGGCTGGTGAAGACAATAATTATTAATTCG 540
Db 481 GGAAGGCTGTGAGTGGCTGGGATATATGGGCTGGTGAAGACAATAATTATTAATTCG 540
Oy 541 GCTCTTATGTCCAGACTGAGCATCAAGAGCAACATCCAAAGCCAAAGTTTCTTAA 600
Db 541 GCTCTTATGTCCAGACTGAGCATCAAGAGCAACATCCAAAGCCAAAGTTTCTTAA 600
Oy 601 ATGAACAGTCTGCAAACTGATGACACAGCCATGTACTCTGCCAGTCCGGGGGTAA 660
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Oy 661 TAGCGCTATGCTTTGGACTACTGGGGTCAAGAACTGACACCGTCTCTCA 714
Db 661 TAGCGCTATGCTTTGGACTACTGGGGTCAAGAACTGACACCGTCTCTCA 714
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ID	ADQ91081	standard; DNA; 1479 BP.
XX	ADQ91081;	
XX	23-SEP-2004	(first entry)
XX	Antibody scFv EPCAMxCD3 with M1 mutant in anti CD3 region encoding DNA.	
XX	CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;	
KW	immunosuppressive; proliferative disease; tumour; inflammatory disease;	
KW	immunological disorder; autoimmune disease; infectious disease;	
XX	scFv EPCAMxCD3; antibody; ds.	
XX	Synthetic.	
OS	Unidentified.	
XX	Key	Location/Qualifiers
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FT		/product= "scFv EPCAMxCD3 with M1 mutant in anti CD3 region"
FT		/note= "No start codon"
XX	CA2403313-A1.	
XX	11-APR-2004.	
PD	11-OCT-2002; 2002CA-02403313.	
XX	11-OCT-2002; 2002CA-02403313.	
XX	11-OCT-2002; 2002CA-02403313.	
PR	(MICR-) MICROMET AG.	
XX	Lanzavecchia A;	
PI	WPI; 2004-390792/37.	
DR	P-PSDB; ADQ91080.	
XX	Antibody construct, useful in treating, e.g., cancer and inflammatory	
PT	diseases comprises at least one mutated CDR3 region.	
XX	Claim 22; SEQ ID NO 62; 80pp; English.	
PS	The invention relates to a novel polypeptide construct comprising at	
XX	least one CDR3 region comprising at least one mutation in a fully defined	
CC	sequence of 6 amino acids. A construct of the invention has	
CC	antiinflammatory, antimicrobial, cytostatic, immunomodulator, and	
CC	immunosuppressive activity. The polypeptide construct, polynucleotide,	
CC	vector or composition are useful for the prevention, treatment or	
CC	amelioration of a proliferative disease, a tumorous disease, an	
CC	inflammatory disease, an immunological disorder, an autoimmune disease or	
CC	an infectious disease in a human subject. The present sequence encodes	
CC	bispecific single chain antibody scFv EPCAMxCD3 with the M1 mutant	
CC	peptide in the anti CD3 region.	
XX	Sequence 1479 BP; 385 A; 365 C; 389 G; 340 T; 0 U; 0 Other;	
SO	Query Match	67.2%; Score 480; DB 12; Length 1479;
	Best Local Similarity	81.5%; Pred. No. 1.9e-129;
	Matches 587; Conservative	0; Mismatches 115; Indels 18; Gaps 2
OY	3 TATTGTGATGACCCAGACTCCCAAAATTCCTGCTTGATATGACAGAGAGAGGGTTACAT	62
DB	3 TATCCAGCTGACCCAGCTCAAAAATTCATGTCCACATCAGTAGAGAGACAGGGTCAAGCCT	62
OY	63 AACCTGCAAGGGCAGTGCAGAGTGTGAGTAATGATGAGCTTGATCCAAACAGAGCGAGG	122
DB	63 CACCTGCAAGGGCAGTGCAGAGTGTGAGTAATGATGAGCTTGATCCAAACAGAGCGAGG	122
OY	123 GCAGTCTCCGAAACTGCTGATATTACTCTGCATCCAAATCGTCACTGAGTCCCTGATG	182

Db	123	GCATCTCTTAAAGCATGATTTACTTCGGCATCTTACCGGTACAGTGGAGTCCCTATCG	182
Qy	183	CTTCACTGGCAGTGGATATATGGACCGAATTTCACTTTCACATTCAGCATCTGTGACAGCTGA	242
Db	183	CTTCAAGGCACTGATCTCGGACACAGATTTTCACTCTCACCAATCAGCAATGTGCAGTCTGA	242
Qy	243	AGACTGSCAGTTTATTTCTGTGTGACAGAGATTAATAGCT-----GCGTGGAGGGG	293
Db	243	AGACTTGGCAGAGTATTTCTGTGCACCAATATATAACAGCTATCCGCTACCGTTCGGTCTCG	302
Qy	294	GACCAAGCTCGAAATATAAAGGTGGAGGCGGCTTCAGCGGAGGTGGCTCTGGCGGTGGCGG	353
Db	303	GACCAAGCTCGAGATCAAAAGGTGGTGGTGTCTGGCGGCGGCGGCTTCGGTGGTGGTGG	362
Qy	354	ATCGCAGGTGCGAGTGAAGAAGATCAGACCTGGCTGGTGGCGGCTTCACAGAGCTGTTC	413
Db	353	TTCTTAGGTGAAACCTGCAGAGATCAGAGACTGGCTTAAGTCAGACCTTCACAGAGCTGTTC	422
Qy	414	CATCACTTGACCTGTCTGTGGTTTTCATTAAACCAATTATGGTGTACACTGGGTTTGGCA	473
Db	423	CATCACTTGACAGATCTGTGGTTTTCATTAACTAGCTATGGTGTACACTGGGTTTGGCA	482
Qy	474	GCCTTCAGAAAAGGCTCTGGAATGGCTGGGAGTATATATGGCTGGTGGAAACCAATTA	533
Db	483	GTCTTCAGAAAAGGCTCTGGAATGGCTGGGAGTGTATATGGATGTGGAAAGCACACACTA	542
Qy	534	TAAATCGGCTCTTATGTCCAGACTGAGCATCAGCAAGACACTCCAGAGCCAAATTTT	593
Db	543	TAACTAGCTTTCAATATCACTAGACTAGCATCAGCAAGACAAATTCAGAGCCAAATTTT	602
Qy	594	CTTAAAAATGAACAGCTGTGCAAACTGATATGACACAGCCATATATCTATGTGCCAGTGGG	653
Db	603	CTTAAAAATGAACAGCTGTGCAAGCTATATATGACACAGCCATATATCTATGTGCCAGATGG	661
Qy	654	GGGTACTACAGGCTATGCTTTGGACTATCTGGGGTCAAGGAACCTCAGTCAAGCTCTCCTC	713
Db	662	-----AGAACTGTGTGTTTGTCTACTGTGGGGCAAGGAGCAACGTCACCGCTCTCTC	713
RESULT 5			
ID	ADQ91091	standard; DNA, 1479 BP.	
XX	AC	ADQ91091;	
XX	DT	23-SEP-2004 (first entry)	
DE	XX	Antibody scFv EpcAMKCD3 with M1 mutant in anti CD3 region encoding DNA.	
XX	XX	CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;	
KW	KW	immunosuppressive; proliferative disease; tumour; inflammatory disease;	
KW	KW	immunological disorder; autoimmune disease; infectious disease;	
XX	XX	scFv EpcAMKCD3; antibody; ds.	
OS	XX	Synthetic.	
OS	XX	Unidentified.	
PH	Key	Location/Qualifiers	
FT	FT	1..1479	
FT	FT	/*tag= a	
FT	FT	/product= "scFv EpcAMKCD3 with M1 mutant in anti CD3	
FT	FT	region"	
FT	FT	/note= "No start codon"	
FT	FT	/transl_except= (pos:625..627,aa:Ala)	
XX	PN	CA2403313-Al.	
XX	PD	11-APR-2004.	
XX	PF	11-OCT-2002; 2002CA-02403313.	
XX	PR	11-OCT-2002; 2002CA-02403313.	

XX (MICR-) MICROMET AG.
 PA
 XX Lanzavecchia A;
 PI
 XX WPI: 2004-390792/37.
 DR P-PSDB; ADQ91090.
 DR
 XX
 PT Antibody construct, useful in treating, e.g., cancer and inflammatory
 PT diseases comprises at least one mutated CDR3 region.
 PS
 XX Claim 22; SEQ ID NO 72; 80bp; English.
 CC The invention relates to a novel polypeptide construct comprising at
 CC least one CDR3 region comprising at least one mutation in a fully defined
 CC sequence of 6 amino acids. A construct of the invention has
 CC anti-inflammatory, antimicrobial, cytostatic, immunomodulator, and
 CC immunosuppressive activity. The polypeptide construct, polynucleotide,
 CC vector or composition are useful for the prevention, treatment or
 CC amelioration of a proliferative disease, a tumorous disease, an
 CC inflammatory disease, an immunological disorder, an autoimmune disease or
 CC an infectious disease in a human subject. The present sequence encodes
 CC bispecific single chain antibody scFv EpCAMxCD3 with the M11 mutant
 CC peptide in the anti CD3 region.
 XX
 SQ Sequence 1479 BP; 385 A; 365 C; 387 G; 342 T; 0 U; 0 Other;
 Query Match 67.2%; Score 480; DB 12; Length 1479;
 Best Local Similarity 81.5%; Pred. No. 1.9e-129;
 Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;
 QY 3 TATGTGATGACCCAGACTCCCAATTCCTGCTGTATCAGCAGAGACAGGGTTACAT 62
 DB 3 TATCCACCTGACCCAGTCTCAAAATTCATGTCCACATCAGTAGAGCAGGGTACAGCGT 62
 QY 63 AACCTGCAAGGCCAGTGCAGAGTGAATGATGATGCTGGCTGTACCAAGAGACCG 122
 DB 63 CACCTGCAAGGCCAGTGCAGAGTGAATGATGATGCTGGCTGTACCAAGAGACCG 122
 QY 123 GCACTCTCCGAACTGTGATATCTGATTCATCCATGCTACATGAGTCCCTGATCG 182
 DB 123 GCAATCTCTTAAACACTGATTTACTCGGCATCTTACCGGTACAGTGGAGTCCCTGATCG 182
 QY 183 CTTCACCTGGAGTGAATGAGGAGATTTCACTTACCTACCACTGCTGACGCTGCA 242
 DB 183 CTTCACCTGGAGTGAATGAGGAGATTTCACTTACCTACCACTGCTGACGCTGCA 242
 QY 243 AGACCTGGCAGTTTATTTCTGTGACAGAGATTATAGCT-----CGCTCGAGGGGG 293
 DB 243 AGACTTGGCAGATTAATTTCTGTGACAGATTAATTAACGCTATCCGCTCAGCTTGGTCTGG 302
 QY 294 GACCAAGCTGGAAATAAAGGTGAGGCGGTTTCAGGCGGAGGTGGCTTGGCGGTGGCGG 353
 DB 303 GACCAAGCTGGAGATCAAAAGGTGAGGCGGTTTCAGGCGGAGGTGGCTTGGCGGTGGCGG 362
 QY 354 ATGCCAGGTGAGTGAAGAGTCAAGACCTGGCTGGTGGCGGCTTACAGAGCCTGTCTC 413
 DB 363 TTTCAGAGTGAATTCGACGAGAGTCAAGACCTGGCTGGTGGCGGCTTACAGAGCCTGTCTC 422
 QY 414 CATCACTGCACTGCTCTCTGGGTTTTCATTAACCAATTAAGTGTGACCTGGGTTTCGCA 473
 DB 423 CATCACTGCACTGCTCTCTGGGTTTTCATTAACCTAGCTATGATGATGACCTGGGTTTCGCA 482
 QY 474 GCTTCAGAAAGGCTGAGTGGCTGGAGTGAATATGAGTGGTGGAGACCAAAATTA 533
 DB 483 GCTTCAGAAAGGCTGAGTGGCTGGAGTGAATATGAGTGGTGGAGACCAAGACTA 542
 QY 534 TAAATCGGCTTTATGTCACAGTGAAGATCAGCAAGACCAACTCCAAAGACCAAGTTT 593
 DB 543 TAAATCGGCTTTATGTCACAGTGAAGATCAGCAAGACCAACTCCAAAGACCAAGTTT 602
 QY 594 CTTAAATGAAGAGTGTGCAAACTGATGACAGAGCATGTACTGCTGCAAGTGGGG 653

DB 603 CTTAAATGAAGAGTGTGCAAACTGATTAAGACAGCATATATTACTGTGCCAGATGG- 661
 QY 654 GGGTAAGTACGCTATCTTGGACTATGCGGGTCAAGAACTCAGTCAACCGTCTCTC 713
 DB 662 -----AGAACTGTGCTTGTCTTACTGGGGCAAGAGACACAGGTCAACCGTCTCTC 713
 RESULT 6
 ADQ91105
 ID ADQ91105 standard; DNA; 1479 BP.
 XX
 AC ADQ91105;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Antibody scFv EpCAMxCD3 with M69 mutant in anti CD3 region encoding DNA.
 XX
 KW CDR3; anti-inflammatory; antimicrobial; cytostatic; immunomodulator;
 KW immunosuppressive; proliferative disease; tumour; inflammatory disease;
 KW immunological disorder; autoimmune disease; infectious disease;
 KW scFv EpCAMxCD3; antibody; ds.
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1479
 FT /*tag= a
 FT /product= "scFv EpCAMxCD3 with M69 mutant in anti CD3
 FT region"
 FT /note= "No start codon"
 FT /transl_except= (pos:1054..1056,aa:Tyr)
 FT
 XX CA2403313-A1.
 XX
 XX 11-APR-2004.
 XX
 XX 11-OCT-2002; 2002CA-02403313.
 XX
 XX 11-OCT-2002; 2002CA-02403313.
 XX
 XX (MICR-) MICROMET AG.
 XX
 XX Lanzavecchia A;
 XX
 XX WPI: 2004-390792/37.
 DR P-PSDB; ADQ91104.
 DR
 XX
 PT Antibody construct, useful in treating, e.g., cancer and inflammatory
 PT diseases comprises at least one mutated CDR3 region.
 PS
 XX Claim 22; SEQ ID NO 86; 80bp; English.
 CC The invention relates to a novel polypeptide construct comprising at
 CC least one CDR3 region comprising at least one mutation in a fully defined
 CC sequence of 6 amino acids. A construct of the invention has
 CC anti-inflammatory, antimicrobial, cytostatic, immunomodulator, and
 CC immunosuppressive activity. The polypeptide construct, polynucleotide,
 CC vector or composition are useful for the prevention, treatment or
 CC amelioration of a proliferative disease, a tumorous disease, an
 CC inflammatory disease, an immunological disorder, an autoimmune disease or
 CC an infectious disease in a human subject. The present sequence encodes
 CC bispecific single chain antibody scFv EpCAMxCD3 with the M69 mutant
 CC peptide in the anti CD3 region.
 XX
 SQ Sequence 1479 BP; 387 A; 364 C; 389 G; 339 T; 0 U; 0 Other;
 Query Match 67.2%; Score 480; DB 12; Length 1479;
 Best Local Similarity 81.5%; Pred. No. 1.9e-129;
 Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;
 QY 3 TATGTGATGACCCAGACTCCCAATTCCTGCTGTATCAGCAGAGACAGGGTTACAT 62

Db	3	TATCCAGCTGACCCGAGCTCTCAAAAATTCATGTCCACATCATGATGAGGACGAGGTCAGGCT	62
Oy	63	AACCTCGAAGCCGACGTCAGAGTGTAGTAAATATATGTGGCTGTGTACCAACGAAGCCAGG	122
Db	63	CACCTGCAAGGCCAGTCAGAAATGTGGGATCTAATATGACCTGTGTATCAACGAAGAACGAGG	122
Oy	123	GCAGTCTCCGAAACCTGCTGATATATCTCTCATCCATCGCTACACTGAGATCCCTGATCG	182
Db	123	GCATCTCTTAAAGACGTATGATTTATCTCGGCATCTTACCGGTATCAGTGGAGTCCCTGATCG	182
Oy	183	CTTCACTGGCAGTGGATATATGGGACGGATTTCACTTTCAACATCAGACCTGTGCAGCTGA	242
Db	183	CTTCAACAGGACGTGGATCTGGGACAGATTTCACTCTCAACATCAGCAATGTGCAGTCTGA	242
Oy	243	AGACCTGGCAGTTTATTTCTGTGCAGGAGATTAATAGCT-----CGCTCGGAGGGGG	293
Db	243	AGATCTGGCAGAGTATTTCTGTGCAGAAATATACGATCTATCCGCTCAAGTTTCGTGGCTGG	302
Oy	294	GACCAAGCTGGAAATATTAAGGTGAGGCCGTTCAAGCGAGAGTGGCTCTGGCGGTGGCGG	353
Db	303	GACCAAGCTCGAATCATAAAGTGGTGGTGGTTCTGGCGGCGGCGGCTCGGTTGGTGGTGG	362
Oy	354	ATGCAAGGTGCAGGTGAAGAGTCAAGAACTTGCCCTGGTGGGCCCTTCAACAGACCTGTG	413
Db	363	TTCTCAGGTGAAACTCAGAGATCAGAGACCTGGCTTAATGTGACGCCCTCAACAGACCTGTG	422
Oy	414	CATCACTTGACGTCTCTGGGTTTTCAATTAACAATATGSGTGTACACTGGGTTGGCA	473
Db	423	CATCACTTGACAGTCTCTGGTTTTCTCAATTAAGCTATGGTGTACACTGGGTTGGCA	482
Oy	474	GCCCTCAGGAAAGGTTCTGAGTGGCTGGAGTAATATGGCTGGTGGAGCACAAAATTA	533
Db	483	GTCTCCAGGAAAGGTTCTGAGTGGCTGGAGTGTGATATGAGTGGTGGAAACAGACTA	542
Oy	534	TAAATTTGGGCTCTAATGTCCAGACTAGACATCAGCAAGACAACCTCCAAAGACCAAGTTT	593
Db	543	TAAATGAGCTTTATATCCAGATGACATCAGCAAGACAACATTCCAAAGACCAAGTTTT	602
Oy	594	CTTAAAAATGACAGTCTGCAAACTGATGACACAGCCATGTACTACTGTGCGAGTCGAGG	653
Db	603	CTTAAAAATGACAGTCTGCAAGCTATGACACAGCCATATTTATCTGTGCAAAATGG-	661
Oy	654	GGGTAATACGCGCTATGCTTTGGACTACTCTGGGGTCAAGAACTCAGTCAACCGTCTCTC	713
Db	662	-----AAMACTGTGTGCTTGTCTTACATGGGGCCAAAGGACACAGGTCAACCGTCTCTC	713

RESULT	7
ADQ91079	
ID	ADQ91079 standard; DNA; 1479 BP.
XX	
AC	ADQ91079;
XX	
DT	23-SEP-2004 (first entry)
XX	
DE	Bispecific single chain antibody scFv EpcAMxCD3 SRQ ID NO:60.
XX	
KW	CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;
KW	immunosuppressive; proliferative disease; tumor; inflammatory disease;
KW	immunological disorder; autoimmune disease; infectious disease;
scFv	EpcAMxCD3; antibody; ds.
XX	
OS	Synthetic.
OS	unidentified.
XX	
FH	Key
FT	CDS
FT	
FT	
XX	
PN	CA2403313-A1.

PD 11-APR-2004.
XX
PF 11-OCT-2002; 2002CA-02403313.
XX
PR 11-OCT-2002; 2002CA-02403313.
XX
PA (MICR-) MICROMET AG.
XX
PI Lanzavecchia A;
XX
WP; 2004-390792/37.
DR
P-PSDB; ADQ91078.
XX
PT Antibody construct, useful in treating, e.g., cancer and inflammatory
PT diseases comprises at least one mutated CDR3 region.
XX
PS
PS Example 7; SEQ ID NO 60; 80pp; English.
XX
XX The invention relates to a novel polypeptide construct comprising at
CC least one CDR3 region comprising at least one mutation in a fully defined
CC sequence of 6 amino acids. A construct of the invention has
CC antiinflammatory, antimicrobial, cytostatic, immunomodulator, and
CC immunosuppressive activity. The polypeptide construct, polynucleotide,
CC vector or composition are useful for the prevention, treatment or
CC amelioration of a proliferative disease, a tumorous disease, an
CC inflammatory disease, an immunological disorder, an autoimmune disease or
CC an infectious disease in a human subject. The present sequence encodes
CC bispecific single chain antibody scfv BpCAMxKD3.
XX
XQ Sequence 1479 BP; 385 A; 364 C; 389 G; 341 T; 0 U; 0 Other;

Query Match	67.2%	Score	480	DB	12	Length	1479		
Best Local Similarity	81.5%	Pred.	No	1.9e-129					
Matches	587	Conservative	0	Mismatches	115	Indels	18	Gaps	2

Qy	3	TAATGTGATGATGCCAGACTCCCAATTTCCTGCTTGATACAGCAGAGACAGGGTTACAT	62
Db	3	TATCCACGTGACCCAGACTCCAAAATTCATGTCACATCACTAGAGAGCAGGGTCAAGGT	62
Qy	63	AACCTGCAAGGCCAGTGCAGAGTGTGATTAATGATGTGGCTTGTTACCAACAGAACCCAG	122
Db	63	CACCTGCAAGGCCAGTGCAGATGTGGGTACTAAATGTAAGCTTGTTATCAACAGAAACCAAG	122
Qy	123	GCAGTCTCCGAACTGCTGATATATCTGTGCATCCAAATCGCTTACACTGAGTCCCTGATCG	182
Db	123	GCAATCTCCTAAGACACTGATTTTACTCGGCACTCCACGGATACAGTGAAGTCCCTGATCG	182
Qy	183	CTTCACGTGGCAGTGGATATGGAAGGATTTCACTTCAACATTCAGCACTGTGACAGGCTGA	242
Db	183	CTTCACAGGCAGTGGATCTGGGACAGATTTCACTCAACATTCAGCAATGTGCACTGTGA	242
Qy	243	AGACCTGGCAGTTTATTTCTGTGCAGCAGATTATAGCT-----CGCTCGAGGGGG	293
Db	243	AGACTTGGCAGAGATTTTCTGTGCAGCAATTAAACAGTATCCGCTCAAGTTCCGGTCTGG	302
Qy	294	GACCAACTGGAAATAAAGGTGAGGCGGTTACAGCGGAGGTGGCTTGGCGGTGGGG	353
Db	303	GACCAACTGGAGATCAAAAGGTGTGTGTCTTCGCGCGCGCGGCTTCGGTGTGTGG	362
Qy	354	ATCGCAGGTGCAGGTGAAGAGTGCAGACCTGGCCTGTGTGGCGGCTTCACAGAGCTGTTC	413
Db	363	TTCTCAGGTGAATGTGAGAGGTGAGGACCTGGCTGTGTGAGGCGCTTCACAGAGCTGTTC	422
Qy	414	CATCACTTGCACTGTCTCTGGGTTTTCATTAACAAATTATGTGTACACTGGGTTCCGCA	473
Db	423	CATCACTTGCACACTCTCTGTGTTTTCTATTAACTAGCTATGTGTATCACTGGTTCGCA	482
Qy	474	GCCCTCAGAAAGGGTCTGAGTGGCTGGGAGTATATGGCTGGTGAACACAAATTA	533
Db	483	GTCCTCAGAAAGGGTCTGAGTGGCTGGGAGTATATGAGTGTGTGAACACAGACTA	542
Qy	534	TAATTGGCTCTTATGTCCAGACTGAGCATCAGCAAGACCAATTCGAAGCCAAATTTT	593

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Db 543 TAATGACGCTTCATATCCAGACTGAGCATCAGCAAGGCAATTCGAAGCCAAAGTTT 602
QY 594 CTTAAATATGAACAGTCTGCAAACTGATGACACAGCCATGTACTCTGTCCAGTCGGG 653
Db 603 CTTTAAATGAACAGTCTGCAAGCTAAATGACACAGCCATATATTACTGTGCGCAATG- 661
QY 654 GGGTAACTACGCTATGCTTTGGAAGTCTGAGGAGTCAAGAACTCAGTACCGTCTCTC 713
Db 662 -----AGAACTGTGCTTTGCTTACTGAGGCGCAAGGACCAAGTCACCGTCTCTC 713

RESULT 8
ADS99440 standard; DNA; 1479 BP.
AC ADS99440;
XX 02-DEC-2004 (first entry)
DT Antibody scFv EpcAMxCD3 with M13 mutant in anti CD3 region encoding DNA.
XX CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;
KW immunosuppressive; proliferative disease; tumour; inflammatory disease;
KW immunological disorder; autoimmune disease; infectious disease;
KW scFv EpcAMxCD3; antibody; ds.
XX Synthetic.
OS Unidentified.
FH Key Location/Qualifiers
FT 1.1479
FT CDS /tag= a
FT /product= "scFv EpcAMxCD3 with M13 mutant in anti CD3
FT region"
FT /note= "No start codon"
XX CA2403313-A1.
PN 11-APR-2004.
XX 11-OCT-2002; 2002CA-02403313.
XX 11-OCT-2002; 2002CA-02403313.
XX PR 11-OCT-2002; 2002CA-02403313.
XX PA (MICR-) MICROMET AG.
XX PI Lanzavecchia A;
XX WPI: 2004-390792/37.
XX P-PSDB; ADS99439.
DR Antibody construct, useful in treating, e.g., cancer and inflammatory
FT diseases comprises at least one mutated CDR3 region.
XX Claim 22; SEQ ID NO 74; 80bp; English.
XX The invention relates to a novel polypeptide construct comprising at
CC least one CDR3 region comprising at least one mutation in a fully defined
CC sequence of 6 amino acids. A construct of the invention has
CC antiinflammatory, antimicrobial, cytostatic, immunomodulator, and
CC immunosuppressive activity. The polypeptide construct, polynucleotide,
CC vector or composition are useful for the prevention, treatment or
CC amelioration of a proliferative disease, a tumorous disease or
CC inflammatory disease, an immunological disorder, an autoimmune disease or
CC an infectious disease in a human subject. The present sequence encodes
CC bioprecific single chain antibody scFv EpcAMxCD3 with the M13 mutant
CC peptide in the anti CD3 region.
XX Sequence 1479 BP; 387 A; 364 C; 388 G; 340 T; 0 U; 0 Other;
SO Query Match 67.2%; Score 480; DB 13; Length 1479;
Beat Local Similarity 81.5%; Pred. No. 1.9e-129;
Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;
```

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QY 3 TATGTGATGACCCAGACTCCCAATTCCTGCTGTATACGACAGAGACAGGGTTACAT 62
Db 3 TATCAGGTGACCCAGTCTCAAAAATTCATGTCACATCATGATAGAGACAGGGTCAGGT 62
QY 63 AACCTGCAAGGCCAGTACAGTGTGATTAATGATGTGGCTTGTACCAACAGAACCCAG 122
Db 63 CACCTGCAAGGCCAGTACAGATGTGGGTATCTAATGTAGCCCTGTATCAACGAAACAG 122
QY 123 GCAGTCTCCGAACTGCTGATATACCTGCATTCATTCGCTACACTGAGTCCCTGATCG 182
Db 123 GCAATCTCTTAAACACTGATTTTACTCGGCATCTTACCGGTACAGTGAAGTCCCTGATCG 182
QY 183 CTTGACCTGGCAGTGGATATGAGGAGGATTTTCACTTACATTCAGCATCTGAGCGAGCTGA 242
Db 183 CTTGACAGGACGTGATCTGGGACAGATTTTACTCTCACTCACTACGCAATGTGCACTTGA 242
QY 243 AGACCTGGCAGTTTATTTCTGTGACAGATTTATAGCT-----CGCTCGAGAGGAGG 293
Db 243 AGACTTGGCAGAGTATTTCTGTGACAGATTTATACAGCTATTCGCTCAGCTTGGTCTCG 302
QY 294 GACCAAGCTGAAATTAAGGTGAGCGGTTCAAGCGGAGTGGCTTGGCGGTCGCG 353
Db 303 GACCAAGCTGAGATCAAAAGGTGGTGGTCTGGCGCGCGGCTCCGGTGGTGGTGG 362
QY 354 ATGCGAGGTGAGGTGAAGAGTACAGAGACCTGGCTGGTGGCGGCTTCAAGACCTGTG 413
Db 363 TTTCAGGTGAATCGACAGAGTACAGACCTGGCTGTAGTGCAGCCCTTCAAGACCTGTG 422
QY 414 CATCACTTGCACCTGTCTGTGGTTTTCATTAAACCAATTATGTGTACACTGGGTTCCCA 473
Db 423 CATCACTTGCACAGTCTGTGGTTTTCATTAACTAGCTATGTGTACACTGGGTTCCCA 482
QY 474 GCCTTCAGAAAGGCTGTGAGTGGCTGGGAGTAAATGCGCTGTGAAACACAAATTA 533
Db 483 GTCTCCAGAAAGGCTGTGAGTGGCTGGGAGTAAATGAGTGTGAAACACACACTA 542
QY 534 TAATTCGGCTCTTATGTCCAGACTGACATTCAGAAAGCAACTCCAAAGCCAAATTT 593
Db 543 TAATGACGCTTTCATATCCAGACTGACATTCAGAAAGCAACTCCAAAGCCAAATTT 602
QY 594 CTTAAATATGAACAGTCTGCAAACTGATGACAGCCATGACTACTGTGCGCAGTCGGG 653
Db 603 CTTTAAATGAACAGTCTGCAAGCTTAATGACAGCCATATATTACTGTGCGCAATG- 661
QY 654 GGGTAACTACGCTATGCTTTGGAAGTCTGAGGAGTCAAGAACTCAGTACCGTCTCTC 713
Db 662 -----AGAACTGTGCTTTGCTTACTGAGGCGCAAGGACCAAGTCACCGTCTCTC 713

RESULT 9
ADS99446 standard; DNA; 1479 BP.
ID ADS99446
XX ADS99446;
XX 02-DEC-2004 (first entry)
DT Antibody scFv EpcAMxCD3 with M31 mutant in anti CD3 region encoding DNA.
XX CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;
KW immunosuppressive; proliferative disease; tumour; inflammatory disease;
KW immunological disorder; autoimmune disease; infectious disease;
KW scFv EpcAMxCD3; antibody; ds.
XX Synthetic.
OS Unidentified.
FH Key Location/Qualifiers
FT 1.1479
FT CDS /tag= a
FT /product= "scFv EpcAMxCD3 with M31 mutant in anti CD3
FT region"
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QY 414 CATCATCTGACATGCTCTGCGGTTTTCATTAAACCAATTATGATGACATGCGGTTCCCA 473
Db 423 CATACCTGACAGTCTCTGTTTCTCATTTAAGTATAGTGTACACTGGGTTGCCA 482
QY 474 GCTCCAGGAAAGGCTTGGAGTGGCTGGGAGTATATGCGCTGGTGGAAACCAATT 533
Db 483 GTCTCCAGGAAAGGCTTGGAGTGGCTGGGAGTATATGCGCTGGTGGAAACCAACT 542
QY 534 TAAATGGGCTCTTATGTCAGACTGAGCATCAGCAAGACATCCCAAGGCAAGTTT 593
Db 543 TAAATGGGCTCTTATGTCAGACTGAGCATCAGCAAGACATCCCAAGGCAAGTTT 602
QY 594 CTTAAATGAAACAGTCTGCAAACTGATGACAGCCATGACTCTGTCAGTCGCGG 653
Db 603 CTTTAAATGAAACAGTCTGCAAACTGATGACAGCCATGACTCTGTCAGTCGCGG- 661
QY 654 GGGTAACTAGCGCTATGCTTTGAGACTCTGGGGTCAAGGAACCTCACTCCGTTCTC 713
Db 662 -----AGAACTGGTGGTTGCTTAACTGGGGCCAAAGGACCAAGGTCACCGTCTCTC 713

RESULT 12

ADSS99430 standard; DNA; 1479 BP.

ADSS99430;

02-DEC-2004 (first entry)

Antibody scFv BpCMxCD3 with M4 mutant in anti CD3 region encoding DNA.

CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;

immunosuppressive; proliferative disease; tumour; inflammatory disease;

immunological disorder; autoimmune disease; infectious disease;

scFv BpCMxCD3; antibody; ds.

Synthetic.

Unidentified.

Key Location/Qualifiers

CA2403313-A1.

11-APR-2004.

11-OCT-2002; 2002CA-02403313.

11-OCT-2002; 2002CA-02403313.

(MICR-) MICROMET AG.

Lanzavecchia A;

WPI; 2004-390792/37.

P-PSDB; ADSS99429.

Antibody construct, useful in treating, e.g., cancer and inflammatory

diseases comprises at least one mutated CDR3 region.

Claim 22; SEQ ID NO 64; 80pp; English.

The invention relates to a novel polypeptide construct comprising at

least one CDR3 region comprising at least one mutation in a fully defined

sequence of 6 amino acids. A construct of the invention has

antiinflammatory, antimicrobial, cytostatic, immunomodulator, and

immunosuppressive activity. The polypeptide construct, polynucleotide,

vector or composition are useful for the prevention, treatment or

CC inflammatory disease, an immunological disorder, an autoimmune disease or

CC an infectious disease in a human subject. The present sequence encodes

CC bispecific single chain antibody scFv BpCMxCD3 with the M4 mutant

CC peptide in the anti CD3 region.

XX Sequence 1479 BP; 385 A; 364 C; 390 G; 340 T; 0 U; 0 Other;

Query Match 67.2%; Score 480; DB 13; Length 1479;

Best Local Similarity 81.5%; Pred. No. 1.9e-129;

Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

QY 3 TATTTGATGACCCAGACTCCCAATTCCTGTTGATGACGAGACAGGGTTACAT 62

Db 3 TATTCAGCTGACCCAGACTCCCAATTCATATGTCACATCAGTGAAGAGGGTCAAGCT 62

QY 63 AACCTGCAAGCCAGTCAAGTGTGATATATGTTGGTGTGTACCAACAAGGACAG 122

Db 63 CACCTGCAAGCCAGTCAAGTGTGATATATGTTGGTGTGTACCAACAAGGACAG 122

QY 123 GCAGTCTCCGAAACTGCTGATATATCTGTGATCATCTGATCATCTGAGTCCCTGATCG 182

Db 123 GCATCTCTTAAAGCACTGATTTTACTCGCATCTTACCGTACAGTGAAGTCCCTGATCG 182

QY 183 CTTTCACTGCGAGTATGATGATGAGCGGATTTCACTTTCACCATCAGCACTGTGAGGCTGA 242

Db 183 CTTCAAGGCAAGTATGATGATGAGCGGATTTCACTTTCACCATCAGCAATGTGAGGCTGA 242

QY 243 AGACCTGGCAAGTTTATTTCTGTGACAGAGATTTAAGT-----CGCTGGAGAGGG 293

Db 243 AGACTTGGCAAGTATTTCTGTGACAGATTTAAGT-----CGCTGGAGAGGG 293

QY 294 GACCAAGCTGGAATTAAGGAGGAGGCGGTTCAAGGCGAGGAGGCTGTGCGGTGAGCG 353

Db 303 GACCAAGCTGGAATTAAGGAGGAGGCGGTTCAAGGCGAGGAGGCTGTGCGGTGAGCG 353

QY 354 ATGCAAGTGTGAGTGAAGAGTCAAGACCTGCGCTGTGCGGCTTCAAGAGCTGTG 413

Db 363 TTCTCAGTGAAGTCAAGTGAAGAGTCAAGACCTGCGCTGTGCGGCTTCAAGAGCTGTG 413

QY 414 CATCATCTGACATGCTCTGCGGTTTTCATTAAACCAATTATGATGACATGCGGTTCCCA 473

Db 423 CATCACTGACAGTCTCTGTTTCTCATTTAAGTATAGTGTACACTGGGTTGCCA 482

QY 474 GCTCCAGGAAAGGCTTGGAGTGGCTGGGAGTATATGCGCTGGTGGAAACCAATT 533

Db 483 GTCTCCAGGAAAGGCTTGGAGTGGCTGGGAGTATATGCGCTGGTGGAAACCAACT 542

QY 534 TAAATGGGCTCTTATGTCAGACTGAGCATCAGCAAGACATCCCAAGGCAAGTTT 593

Db 543 TAAATGGGCTCTTATGTCAGACTGAGCATCAGCAAGACATCCCAAGGCAAGTTT 602

QY 594 CTTAAATGAAACAGTCTGCAAACTGATGACAGCCATGACTCTGTCAGTCGCGG 653

Db 603 CTTTAAATGAAACAGTCTGCAAACTGATGACAGCCATGACTCTGTCAGTCGCGG- 661

QY 654 GGGTAACTAGCGCTATGCTTTGAGACTCTGGGGTCAAGGAACCTCACTCCGTTCTC 713

Db 662 -----AGAACTGGTGGTTGCTTAACTGGGGCCAAAGGACCAAGGTCACCGTCTCTC 713

RESULT 13

ADSS99442 standard; DNA; 1479 BP.

ADSS99442;

02-DEC-2004 (first entry)

Antibody scFv BpCMxCD3 with M14 mutant in anti CD3 region encoding DNA.

CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;

immunosuppressive; proliferative disease; tumour; inflammatory disease;

immunological disorder; autoimmune disease; infectious disease;

KM scFv EpcAMxCD3; antibody; ds.
XX Synthetic.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 1..1479
FT /tag= a
FT /product= "scFv EpcAMxCD3 with M14 mutant in anti CD3
FT region"
FT /note= "No start codon"
PN CA2403313-A1.
PD 11-APR-2004.
XX
XX 11-OCT-2002; 2002CA-02403313.
PF
XX 11-OCT-2002; 2002CA-02403313.
PR
XX (MICR-) MICROMET AG.
PA
XX Lanzavecchia A;
PI
XX WPI: 2004-390792/37.
DR P-PSDB: ADS99441.
XX
XX
PT Antibody construct, useful in treating, e.g., cancer and inflammatory
PT diseases comprises at least one mutated CDR3 region.
XX
XX
PS Claim 22; SEQ ID NO 76; 80bp; English.
XX
XX The invention relates to a novel polypeptide construct comprising at
CC least one CDR3 region comprising at least one mutation in a fully defined
CC sequence of 6 amino acids. A construct of the invention has
CC antiinflammatory, antimicrobial, cytostatic, immunomodulator, and
CC immunosuppressive activity. The polypeptide construct, polynucleotide,
CC vector or composition are useful for the prevention, treatment or
CC amelioration of a proliferative disease, a tumorous disease, an
CC inflammatory disease, an immunological disorder, an autoimmune disease or
CC an infectious disease in a human subject. The present sequence encodes
CC bispecific single chain antibody scFv EpcAMxCD3 with the M14 mutant
CC peptide in the anti CD3 region.
XX
XX
SQ Sequence 1479 BP; 385 A; 364 C; 389 G; 341 T; 0 U; 0 Other;
Query Match 67.2%; Score 480; DB 13; Length 1479;
Best Local Similarity 81.5%; Pred. No. 1.9e-129;
Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;
QY 3 TATTGTGATGACCCAGACTCCCAATTCTGCTGTATACAGAGAGACAGGGTTACCAT 62
DB 3 TATCCAGCTGACCCAGTCTCAAAAATTCATGTCACATCAGTAGAGACAGGGTCAAGCGT 62
QY 63 AACCTGCAAGGCCAGTCAAGTGTGAGTAATGATGCTGCTGTACCAAGAGACCAAG 122
DB 63 CACCTGCAAGGCCAGTCAAGTGTGAGTAATGATGCTGCTGTACCAAGAGACCAAG 122
QY 123 GCACTCTCCGAAACTGCTATATCTGATCCCAATGCTACACTGAGTCCCTGATCG 182
DB 123 GCAATCTCTTAAGACATGATTTACTCGGCATCCACCGGTACAGTGAAGTCCCTGATCG 182
QY 183 CTTTCACTGGCAGTGTGATGTGAGCGAGATTTCATTTCACATCAAGACACTGTGACAGGCTGA 242
DB 183 CTTTCAAGGCGAGTGTGATGTGAGCGAGATTTCATTTCACATCAAGACACTGTGACAGGCTGA 242
QY 243 AGACTGGCACTTTATTTCTGTCTGACAGAGATTATAGCT-----CGCTCCGAGGGGG 293
DB 243 AGACTTGGCAAGATTATTTCTGTCTGACAGAGATTATAGCT-----CGCTCCGAGGGGG 293
QY 294 GACCAAGCTGGAATTAAGAGGTGAGGCGGTTTCAGGCGGAGAGTGTGCTGTGGCGGTGGCGG 353
DB 294 GACCAAGCTGGAATTAAGAGGTGAGGCGGTTTCAGGCGGAGAGTGTGCTGTGGCGGTGGCGG 353
QY 303 GACCAAGCTGGAATTAAGAGGTGAGGCGGTTTCAGGCGGAGAGTGTGCTGTGGCGGTGGCGG 362
DB 303 GACCAAGCTGGAATTAAGAGGTGAGGCGGTTTCAGGCGGAGAGTGTGCTGTGGCGGTGGCGG 362

QY 354 ATGCAGATGCAAGTGAAGAGAGTCAAGACCTGGCCTGTGAGCGCCTCACAAGACCTGTG 413
DB 363 TTCTCAGATGAAGACTGACAGAGATCAGACCTGGCCTGTGAGCGCCTCACAAGACCTGTG 422
QY 414 CATCACTTGCACGTGTCTGTGGGTTTTCATTAAACCAATTATGTGTACACTGTGGTTGCCA 473
DB 423 CATCACTTGCACAGTGTCTGTGGTTCATTAACTAGCTATGTGTACACTGTGGTTGCCA 482
QY 474 GCTTCCAGAAAGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 533
DB 483 GTCTCCAGAAAGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 542
QY 534 TAATTGGCTCTTATGTCCAGACTGACATCAGCAAGCAACTCCCAAGAGCCAAAGTTT 593
DB 543 TAATGAGCTTTCTATATCCAGACTGACATCAGCAAGCAACTCCCAAGAGCCAAAGTTT 602
QY 594 CTTAAATATGAACAGTGTGCAAACTGATGACACAGCCATGTACTGTGTGCAAGTGGGG 653
DB 603 CTTTAAATATGAACAGTGTGCAAGCTATGACACAGCCATGTACTGTGTGCAAGATGG- 661
QY 654 GGGTAATTAAGGCTATGCTTGTGACTGTGGGGTCAAGAACTCACTACCGTCTCTC 713
DB 662 -----AGAACTGTGTGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 713
RESULT 14
ADS99432
ID ADS99432 standard; DNA; 1479 BP.
XX
XX ADS99432;
AC
XX
DT 02-DEC-2004 (first entry)
XX
XX
DE Antibody scFv EpcAMxCD3 with M7 mutant in anti CD3 region encoding DNA.
XX
XX CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;
KM immunosuppressive; proliferative disease; tumour; inflammatory disease;
KM immunological disorder; autoimmune disease; infectious disease;
XX scFv EpcAMxCD3; antibody; ds.
OS Synthetic.
OS Unidentified.
XX
XX
FH Key Location/Qualifiers
FT CDS 1..1479
FT /tag= a
FT /product= "scFv EpcAMxCD3 with M7 mutant in anti CD3
FT region"
FT /note= "No start codon"
PN CA2403313-A1.
PD 11-APR-2004.
XX
XX 11-OCT-2002; 2002CA-02403313.
PF
XX 11-OCT-2002; 2002CA-02403313.
PR
XX (MICR-) MICROMET AG.
PA
XX Lanzavecchia A;
PI
XX WPI: 2004-390792/37.
DR P-PSDB: ADS99431.
XX
XX
PT Antibody construct, useful in treating, e.g., cancer and inflammatory
PT diseases comprises at least one mutated CDR3 region.
XX
XX
PS Claim 22; SEQ ID NO 66; 80bp; English.
XX
XX The invention relates to a novel polypeptide construct comprising at
CC least one CDR3 region comprising at least one mutation in a fully defined


```
Db 243 AGACTTGGCAGAGTATTTCTGTGACGAATATAACAGTATCCGCTCAGCTTCGGTGTGG 302
QY 294 GACCAAGCTGGAATATAAAGGTGAGCGGTTCAAGCCGAGGTGCTCTGGCGGTGGCGG 353
Db 303 GACCAAGCTCAGATCAAAAGGTGGTGTCTGGCGCGCGGCTCCGGTGGTGGTGG 362
QY 354 ATCGAGGTGAGGTGAGAGTCAAGACTGGCCTGGGCGCCCTCACAAGAGCTGTC 413
Db 363 TTCTCAGGTGAACTGCAAGAGTCAAGACTGGCTTAACTGCAAGCCCTCACAAGAGCTGTC 422
QY 414 CATCACTTGCACGTGCTCTGGGTTTTCATTAACCAATTATGGTGTACACTGGGTTGGCCA 473
Db 423 CATCACTGCAAGTCTGCTGGTTTCTCATTTAACTAGCTATGGTGTACACTGGGTTGGCCA 482
QY 474 GCTTCCAGGAAAGGCTCTGGAGTGGCTGGAGTAAATATGGGCTGGTGAAGCACAAATTA 533
Db 483 GTCTCCAGGAAAGGCTCTGGAGTGGCTGGAGTAAATATGGAGTGTGAGACACAGACTA 542
QY 534 TAATTGGGCTCTTAATGTCCAGACTGAGCATCAGCAAGGAACTCCAAAGGCAAGTTT 593
Db 543 TAATGACGCTTTCAATATCAAGACTGAGCATCAGCAAGGAACTCCAAAGGCAAGTTT 602
QY 594 CTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTACTAGTGGCCAGTGGGG 653
Db 603 CTTTAAATGAACAGTCTGCAAGCTAATGACACAGCCATATATTACTGTGCCAAGATGG- 661
QY 654 GGGTAACTACGGCTATGCTTGGACTACTGGGGGTCAAGGAACCTCAGTCAACCGTCTCTC 713
Db 662 -----AGAACTGTGTGTTGTGCTTACTGGGGGCCAAGGGAACAAGGTCAACCGTCTCTC 713
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Search completed: February 18, 2005, 20:38:23
Job time : 422.122 secs

Db 241 GAAGACCTGCGAGTTTATTTCTGTGACAGAGATTATGCTGCTCGAGAGGGGGAGCCAG 300
Qy 301 CTGGAATTAAGGTGAGGCGGTTTCAGGGGAGGTGCTCTGGCGGTGGCGATGCGAG 360
Db 301 CTGGAATTAAGGTGAGGCGGTTTCAGGGGAGGTGCTCTGGCGGTGGCGATGCGAG 360
Qy 361 GTGCAAGTGAAGAGTCAAGACCTGAGCTGTGGCGGCTTCACAGAGCTGTCCATCACT 420
Db 361 GTGCAAGTGAAGAGTCAAGACCTGAGCTGTGGCGGCTTCACAGAGCTGTCCATCACT 420
Qy 421 TGCACTGTCTCTGGGTTTTCATTAAACCAATTATGTGTATCACTGGGTTCCGACCTCCA 480
Db 421 TGCACTGTCTCTGGGTTTTCATTAAACCAATTATGTGTATCACTGGGTTCCGACCTCCA 480
Qy 481 GGAAGGGCTGTGAGTGGCTGGAGTAATATGGGCTGGTGGAAAGCAAAATTAAATTGG 540
Db 481 GGAAGGGCTGTGAGTGGCTGGAGTAATATGGGCTGGTGGAAAGCAAAATTAAATTGG 540
Qy 541 GCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTCCAAAGCCAAAGTTTCTTAAAA 600
Db 541 GCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTCCAAAGCCAAAGTTTCTTAAAA 600
Qy 601 ATGAACAGTCTGCAAACTGATGACACAGCCATGTACTGTGCGAGTGGGGGGGTAAAC 660
Db 601 ATGAACAGTCTGCAAACTGATGACACAGCCATGTACTGTGCGAGTGGGGGGGTAAAC 660
Qy 661 TAGGGCTATGCTTTGAGACTCTGGGGGTCAAGAAACCTCAGTCAACCGTCTCTCA 714
Db 661 TAGGGCTATGCTTTGAGACTCTGGGGGTCAAGAAACCTCAGTCAACCGTCTCTCA 714

RESULT 2

US-09-142-974B-4
; Sequence 4, Application US/09142974B
; Patent No. 6451995
; GENERAL INFORMATION:
; APPLICANT: Cheung, Nai-Kong V.
; APPLICANT: Larson, Steven M.
; APPLICANT: Guo, Hong-Pen
; APPLICANT: Rivlin, Ken
; APPLICANT: Sadelain, Michel
; TITLE OF INVENTION: Single Chain Fv Constructs of Anti-Ganglioside GD2
; FILE REFERENCE: MSK.P-013-USNP
; CURRENT FILING DATE: 1998-09-18
; PRIOR FILING DATE: 1997-03-20
; PRIOR FILING DATE: PCT/US97/04427
; PRIOR APPLICATION NUMBER: 60/013,703
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: 3G6-scFv-streptavidin
US-09-142-974B-4

Query Match 100.0%; Score 714; DB 3; Length 1173;
Best Local Similarity 100.0%; Pred. No. 1,5e-208;
Matches 714; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGTATGTATGATCCAGAGTCCCAAAATTCCTGTTGTATCAGCAGAGACAGGGTTACC 60
Db 1 AGTATGTATGATCCAGAGTCCCAAAATTCCTGTTGTATCAGCAGAGACAGGGTTACC 60
Qy 61 ATAACCTGCAAGGCGAGTCAAGTGTAGTATGATGTGGCTTGGTACCAAGAGGCA 120
Db 61 ATAACCTGCAAGGCGAGTCAAGTGTAGTATGATGTGGCTTGGTACCAAGAGGCA 120

Qy 121 GGGCAGTCTCCGAACTGTGATATATCTGTCAATCGTATCACTGAGTCCCTGAT 180
Db 121 GGGCAGTCTCCGAACTGTGATATATCTGTCAATCGTATCACTGAGTCCCTGAT 180
Qy 181 CGCTTCACTGGCAGTGTATATGGGACGATTTTCACTTTCAACCATCAGCACTGTGACGCT 240
Db 181 CGCTTCACTGGCAGTGTATATGGGACGATTTTCACTTTCAACCATCAGCACTGTGACGCT 240
Qy 241 GAAGACCTGCGACAGTTATTTCTGTGACAGAGATTATAGCTCGCTCGGAGGGGAGCAAG 300
Db 241 GAAGACCTGCGACAGTTATTTCTGTGACAGAGATTATAGCTCGCTCGGAGGGGAGCAAG 300
Qy 301 CTGGAATTAAGGTGAGGCGGTTTCAGGCGAGGTGCTCTGGCGGTGGCGATGCGAG 360
Db 301 CTGGAATTAAGGTGAGGCGGTTTCAGGCGAGGTGCTCTGGCGGTGGCGATGCGAG 360
Qy 361 GTGCAAGTGAAGAGTCAAGACCTGAGCTGTGGCGGCTTCACAGAGCTGTCCATCACT 420
Db 361 GTGCAAGTGAAGAGTCAAGACCTGAGCTGTGGCGGCTTCACAGAGCTGTCCATCACT 420
Qy 421 TGCACTGTCTCTGGGTTTTCATTAAACCAATTATGTGTATCACTGGGTTCCGACCTCCA 480
Db 421 TGCACTGTCTCTGGGTTTTCATTAAACCAATTATGTGTATCACTGGGTTCCGACCTCCA 480
Qy 481 GGAAGGGCTGTGAGTGGCTGGAGTAATATGGGCTGGTGGAAAGCAAAATTAAATTGG 540
Db 481 GGAAGGGCTGTGAGTGGCTGGAGTAATATGGGCTGGTGGAAAGCAAAATTAAATTGG 540
Qy 541 GCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTCCAAAGCCAAAGTTTCTTAAAA 600
Db 541 GCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTCCAAAGCCAAAGTTTCTTAAAA 600
Qy 601 ATGAACAGTCTGCAAACTGATGACACAGCCATGTACTGTGCGAGTGGGGGGGTAAAC 660
Db 601 ATGAACAGTCTGCAAACTGATGACACAGCCATGTACTGTGCGAGTGGGGGGGTAAAC 660
Qy 661 TAGGGCTATGCTTTGAGACTCTGGGGGTCAAGAAACCTCAGTCAACCGTCTCTCA 714
Db 661 TAGGGCTATGCTTTGAGACTCTGGGGGTCAAGAAACCTCAGTCAACCGTCTCTCA 714

RESULT 3

US-08-756-416-31
; Sequence 31, Application US/08756416
; Patent No. 6699715
; GENERAL INFORMATION:
; APPLICANT: Iedebetter, Jeffrey A.
; APPLICANT: Hayden, Martha
; APPLICANT: Fell, Perry
; APPLICANT: Mittleer, Robert
; APPLICANT: Winberg, Gosta
; TITLE OF INVENTION: MODIFIED SPV MOLECULES WHICH
; TITLE OF INVENTION: MEDIANE ADHESION BETWEEN CELLS AND USES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Merchant & Gould
; STREET: 11150 Santa Monica, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/007,755

FILING DATE: 30-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Adriano, Sarah B
 REGISTRATION NUMBER: 34,470
 REFERENCE/DOCKET NUMBER: 30436.41US01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-445-1140
 TELEFAX: 310-445-9031
 TELEX:
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 752 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: Other
 US-08-756-416-31

Query Match 58.0%; Score 414.4; DB 4; Length 752;

Best Local Similarity 76.9%; Pred. No. 8.8e-117; Matches 569; Conservative 0; Mismatches 141; Indels 30; Gaps 4;

QY 4 ATTGTGATGACCCAGACTCCCAAAATTCCTGCTTGATGACGAGACAGGGTTACCAT 63
 DB 7 ATGTGCTCACCCATCTCCAGCTTCTTGCTGTCTTAGAGTCAGAGCCACCATC 66
 QY 64 ACCTGCAAGCCAGTCAGAGTGTGATGATGCTGCT-----TGTACCA 111
 DB 67 TCCGTCAGAGCCAGTGAAGTGTGAATATATGTCAGCAAGTTAATGACGTGTACCA 126
 QY 112 CAGAAGCCAGGCGAGTCTCCGAACTGCTGATATATCTGATCCATCCATCGTACATCGA 171
 DB 127 CAGAAACCCAGGACGACCCCAAACTCTCTGCTGATCCAGTGAATCTGAGG 186
 QY 172 GTCCCTGATCGCTTCACTGCGAGTGAATGAGAGCGAATTCATTTCCATCAGCATG 231
 DB 187 GTCCCTGCGAGTTTATGTCGAGTGGCTCTGGACAGACTTCAGCTCAACATCATCT 246
 QY 232 GTGCAAGCTGAAGACCTGCGAGTTTATTTCTGTACG-----AGGATTAATAGCTG 282
 DB 247 GTGAGGAGGATGATATGCAATGATATTTCTGTGACGAAAGTAGAGAGTCTTGGACG 306
 QY 283 CTGGAGGGGGGAGCAGCTGGAATAAA---GGTGAAGCGGTTACGGGGGAGTGGC 339
 DB 307 TTCTGCTGAGGACAGCAGCTGGAATCAAAAGGGGTGGCTGGGCGGTGGTGG 366
 QY 340 TGTGCGGTGCGGATGCGAGTGCAGGTGAAGAGTCAAGACCTGAGCTGTGGCGCC 399
 DB 367 TCGGCTGCGCGGATCTCAGGTGAGCTGAAGAGTCAAGACCTGAGCTGTGGCGCC 426
 QY 400 TCACAGAGCTGTCCATCATCTTGCATCTGTCTGGGTTTCATTACCAATTATGCTGA 459
 DB 427 TCACAGAGCTGTCCATCATCTTGCATCTGTCTGGGTTTCATTACCAATTATGCTGA 486
 QY 460 CACTGGGTTGGCCAGCTCCAGGAAAGGGTCTGAGGTGGCGGAGTAAATGCGGCTGT 519
 DB 487 AACTGGGTTGGCCAGCTCCAGGAAAGGGTCTGAGGTGGCGGAGTAAATGCGGCTGT 546
 QY 520 GGAAGCAAAATTAATTCGGCTTATGTCAGACTGACATCAGCAAGCAAACTCC 579
 DB 547 GGAAGCAGACCTTAATTCAGCTCTCAATCCAGATCGAGATCAACCAAGCAACTCC 606
 QY 580 AAGGCCAAGTTTCTTAATAATGAACAGTCTGCAACTGATGACACAGCCATGTAATC 639
 DB 607 AAGGCCAAGTTTCTTAATAATGAACAGTCTGCAAACTGATGACACAGCCAGTAATC 666
 QY 640 TGTGCGAGTGGGGGGGTAATC-----GGCTATGCTTGGACTATGGGGTCAAGGA 693
 DB 667 TGTGCGAGATGATGATATGTAATCTTCAATTAATGATGACTACTGGGGTCAAGGA 726
 QY 694 ACTTCAGTCACGCTCTCTCTC 713
 DB 727 ACTTCAGTCACGCTCTCTCTC 746

RESULT 4

US-08-756-416-30

Sequence 30, Application US/08756416

Patent No. 669715

GENERAL INFORMATION:

APPLICANT: Ledbetter, Jeffrey A.

APPLICANT: Hayden, Martha

APPLICANT: Fell, Perry

APPLICANT: Miltner, Robert

APPLICANT: Winberg, Costa

TITLE OF INVENTION: MODIFIED SPV MOLECULES WHICH

TITLE OF INVENTION: MEDIANE ADHESION BETWEEN CELLS AND USES

NUMBER OF INVENTION: 39

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant & Gould

STREET: 1150 Santa Monica, Suite 400

CITY: Los Angeles

STATE: CA

COUNTRY: USA

ZIP: 90025

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/756,416

FILING DATE: 27-NOV-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/007,755

FILING DATE: 30-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Adriano, Sarah B

REGISTRATION NUMBER: 34,470

REFERENCE/DOCKET NUMBER: 30436.41US01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 310-445-1140

TELEFAX: 310-445-9031

TELEX:

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 1509 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: Other

US-08-756-416-30

Query Match 58.0%; Score 414.4; DB 4; Length 1509;

Best Local Similarity 76.9%; Pred. No. 1.2e-116; Matches 569; Conservative 0; Mismatches 141; Indels 30; Gaps 4;

QY 4 ATTGTGATGACCCAGACTCCCAAAATTCCTGCTTGATGACGAGACAGGGTTACCAT 63
 DB 1 ATGTGCTCACCCATCTCCAGCTTCTTGCTGTCTTAGAGTCAGAGCCACCATC 60
 QY 64 ACCTGCAAGCCAGTCAGAGTGTGATGATGCTGCTGCT-----TGTACCA 111
 DB 61 TCCGTCAGAGCCAGTGAAGTGTGAATATATGTCAGCAAGTTAATGACGTGTACCA 120
 QY 112 CAGAAGCCAGGCGAGTCTCCGAAATGCTGATATATCTGATCCATCCATCCATCAGTA 171
 DB 121 CAGAAACCCAGGACGACCCCAAACTCTCATCTGCTGATCAGAGTGAATCTGGG 180
 QY 172 GTCCCTGATGCTTCACTGCGAGTGAATGAGAGCGAATTCACCTTCACATCAGCACT 231
 DB 181 GTCCCTGCGAGTTTATGTCAGAGTGGGTCTGGGACAGACTTCAGCTCAACATCATCT 240
 QY 232 GTGCAAGCTGAAGACCTGCGAGTTTATTTCTGTACG-----AGGATTAATGCTG 282

Db 241 GTGAGAGAGATATATATGCAATCTATTCTGTCAGCAAAAGTAGAAGGTTCTCTGACG 300
QY 283 CTGAGAGGGGAGCAAGCTGGAATATAA--GGTGAAGCGGTTTCAGGCGAGGTGGC 339
Db 301 TTGGGTGAGGACCAAGCTGGAATCAACGGGGTGGCGGTGCTGGGGCGGTGGG 360
QY 340 TCTGGCGGTGGCGGATGCGAGGTGAGAGGATGAGAGCTGGCGGTGGGCGCC 399
Db 361 TCGGTGGCGCGGATCTCAGGTGACGTAAAGAGTCAAGACCTGGCTGGTGGCGCC 420
QY 400 TCACAGAGCTGTCCATCACTTGCACTGTCTGTGGTTTCAATTAACCAATTATGTGTA 459
Db 421 TCACAGAGCTGTCCATCACTTGCACTGTCTGTGGTTTCAATTAACCGGTATGTGTA 480
QY 460 CACTGGGTGGCGGCTCCAGGAAGGTTGAGTGGCTGGGAGTAATGTGGCTGT 519
Db 481 AACTGGGTGGCGGCTCCAGGAAGGTTGAGTGGCTGGGAGTAATGTGGCTGT 540
QY 520 GGAAGCAAAATTAATTTGGGCTTAATGTCAGATGAGCATCAGCAAGGCAACTCC 579
Db 541 GGAAGCAAAATTAATTTGGGCTTAATGTCAGATGAGCATCAGCAAGGCAACTCC 600
QY 580 AAGAGCAAAATTTCTTAATAATGAACAGTCTGCAACTGATGACACAGCCATGTACTAC 639
Db 601 AAGAGCAAAATTTCTTAATAATGAACAGTCTGCAACTGATGACACAGCCATGTACTAC 660
QY 640 TGTGGCGGTGGGGGGGTAACTAC-----GGCTATGCTTTGAGCTATGCGGGTCAAAGA 693
Db 661 TGTGGCGAGATGATTAATGTAATCTTTCATTAATGTATGACTACTGCGGGTCAAAGA 720
QY 694 ACCTCAGTCAACCGTCTCTC 713
Db 721 ACCTCAGTCAACCGTCTCTC 740

RESULT 5
US-08-756-416-29
; Sequence 29, Application US/08756416
; Patent No. 6699715
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha
; APPLICANT: Felt, Perry
; APPLICANT: Mittleer, Robert
; APPLICANT: Winberg, Gosta
; TITLE OF INVENTION: MODIFIED SEV MOLECULES WHICH
; TITLE OF INVENTION: MEDIANE ADHESION BETWEEN CELLS AND USES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,416
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/007,755
; FILING DATE: 30-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Aditiano, Sarah B
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.41US01

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; TELEX:
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1527 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Other
US-08-756-416-29

Query Match 58.0%; Score 414.4; DB 4; Length 1527;
Best Local Similarity 76.9%; Pred. No. 1,2e-116;
Matches 569; Conservative 0; Mismatches 141; Indels 30; Gaps 4;

QY 4 ATTGTATGACCCAGACCTCCCAATTCCGTGTTGATTCAGACAGAGACAGGTTACCAAT 63
Db 1 ATTGTCTCACCACCAATCTCCAGCTTCTTGGCTGTCTGTAGTCAAGAGCCACATC 60
QY 64 ACCTCAAGGCGAGTCAAGTGTGATTAATGATGCT-----TGTACCA 111
Db 61 TCTTCAAGGCGAGTCAAGTGTGATTAATGATGCT-----TGTACCA 120
QY 112 CAGAAAGCGGCGAGTCTCCGAAACGCTGATTAATCTGCAATCCATGCTACACTGA 171
Db 121 CAGAAAGCGGCGAGTCTCCGAAACGCTGATTAATCTGCAATCCATGCTACACTGA 180
QY 121 CAGAAAGCGGCGAGTCTCCGAAACGCTGATTAATCTGCAATCCATGCTACACTGA 180
QY 172 GTCCCTGATCGCTTCACTGCGAGTGAATGAGACGGAATTTCACTTCAACATCAGACT 231
Db 181 GTCCCTGAGAGTTTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 240
QY 232 GTGAGGCTGAAAGACTGGAAGTTATTTCTGTACG-----AGATTAATGACTG 282
Db 241 GTGAGAGAGATGATTAATGCAATGTAATTTCTGTCAAGCAAGTGAAGGTTCTTGAAG 300
QY 283 CTGAGAGGGGAGCAAGCTGGAATAAATAA-----GGTGAAGGGGTTCAAGCGGAGGTGGC 339
Db 301 TTGGGTGAGGACCAAGCTGGAATAAATAAAGGGGTTGAGTGGCTGGGGCGGTGGG 360
QY 340 TGTGGCGGTGGGGGATGCGAGGTGAGAGTGAAGAGTCAAGACTGCGCTGTGGCGCC 399
Db 361 TCGGTGGGGGGGAGTCTCAGGTGAGTGAAGAGTCAAGAGTCTGGCTGGGTGGCGCC 420
QY 400 TCACAGAGCTGTCCATCACTTGCACTGTCTGTGGTTTCAATTAACCAATTATGTGTA 459
Db 421 TCACAGAGCTGTCCATCACTTGCACTGTCTGTGGTTTCAATTAACCGGTATGTGTA 480
QY 460 CACTGGGTGGCGGCTCCAGGAAGGTTGAGTGGCTGGGAGTAATGTGGCTGT 519
Db 481 AACTGGGTGGCGGCTCCAGGAAGGTTGAGTGGCTGGGAGTAATGTGGCTGT 540
QY 520 GGAAGCAAAATTAATTTGGGCTTAATGTCAGATGAGCATCAGCAAGGCAACTCC 579
Db 541 GGAAGCAAAATTAATTTGGGCTTAATGTCAGATGAGCATCAGCAAGGCAACTCC 600
QY 580 AAGAGCAAAATTTCTTAATAATGAACAGTCTGCAACTGATGACACAGCCATGTACTAC 639
Db 601 AAGAGCAAAATTTCTTAATAATGAACAGTCTGCAACTGATGACACAGCCATGTACTAC 660
QY 640 TGTGGCGGTGGGGGGGTAACTAC-----GGCTATGCTTTGAGCTACTGGGGTCAAAGA 693
Db 661 TGTGGCGAGATGATTAATGTAATCTTTCATTAATGTATGACTACTGCGGGTCAAAGA 720
QY 694 ACCTCAGTCAACCGTCTCTC 713
Db 721 ACCTCAGTCAACCGTCTCTC 740

RESULT 6
5455030-16
; Patent No. 5455030

```
APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
POLYPEPTIDE BINDING MOLECULES
NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/40,440
FILING DATE: 1-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 512,910
FILING DATE: 25-APR-1990
APPLICATION NUMBER: 299,617
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 92,110
FILING DATE: 02-SEP-1987
APPLICATION NUMBER: 902,971
FILING DATE: 01-SEP-1986
SEQ ID NO: 16
LENGTH: 729
5455030-16

Query Match      57.2%; Score 408.2; DB 6; Length 729;
Best Local Similarity 75.8%; Pred. No. 6.9e-115;
Matches 548; Conservative 0; Mismatches 163; Indels 12; Gaps 3;

Qy 4 ATTGATGACCCAGACTCCCAATTCTGCTGTATGACGAGAGAGAGGTTACCAT 63
Db 7 AATGTCACCCAGCTCTCCAGCATATGTCGATCTCCAGGGGAAAGATCACATG 66
Qy 64 ACCTGCAAGGCGAGTCAGATGTGAGT---AATGATGTGCTGGTACCAAGAACCA 120
Db 67 ACCTGCAAGGCGAGTCAGATGTGAGT---AATGATGTGCTGGTACCAAGAACCA 126
Qy 121 GGGCAGTCTCCGAAACTGCTGATATCTCTGATCAATCCGTACACTGAGTCCGTGAT 180
Db 127 GGTGCTCTCCGAAACTGCTGATATCTCTGATCAATCCGTACACTGAGTCCGTGAT 186
Qy 181 CGCTTACCTGGCAGTGTATGGGACGAGTTTCACTTTCACATCAGACATGTCAGAGCT 240
Db 187 CGCTTACCTGGCAGTGTATGGGACGAGTTTCACTTTCACATCAGACATGTCAGAGCT 246
Qy 241 GAAGACCTGGCAGTGTATGGGACGAGTTTCACTTTCACATCAGACATGTCAGAGCT 294
Db 247 GAAGACCTGGCAGTGTATGGGACGAGTTTCACTTTCACATCAGACATGTCAGAGCT 306
Qy 295 ACCAAGCTGGAATTAAGATGAGAGCGGTTCAAGCGAGGTGCTGCGGCGGGA 354
Db 307 CCCAAGCTGGAATTAAGATGAGAGCGGTTCAAGCGAGGTGCTGCGGCGGGA 366
Qy 355 TCGCAGGTGCAAGTGAAGAGTCAAGAGCTGCGGCGGCGGCGGCGGCGGCGG 414
Db 367 CTGATGTGCAAGTGAAGAGTCAAGAGCTGCGGCGGCGGCGGCGGCGGCGG 426
Qy 415 ATCACTGCACTGCTCTGGGTTTTCATTAAACAATTAATGATGATCACTGGGTTGCGCAG 474
Db 427 ATCACTGCACTGCTCTGGGTTTTCATTAAACAATTAATGATGATCACTGGGTTGCGCAG 486
Qy 475 CCTCAGAGAAAGGCTCGAGTGTGAGAGTGAATATGAGTGTGAGAGCAAAATAT 534
Db 487 CCTCAGAGAAAGGCTCGAGTGTGAGAGTGAATATGAGTGTGAGAGCAAAATAT 546
Qy 535 AATTCGGCTCTTATGTCCAGACTGAGATCAAGCAAGCAACTCCAAAGCAAGTTTC 594
Db 547 AATTCGGCTCTTATGTCCAGACTGAGATCAAGCAAGCAACTCCAAAGCAAGTTTC 606
Qy 595 TTAATAATGACAGTCTGCAAACTGATGACACAGCAGTACTACTGTCGA---GTGCG 651
Db 607 TTAATAATGACAGTCTGCAAACTGATGACACAGCAGTACTACTGTCGA---GTGCG 666
Qy 652 GGGGGTAACTACGGCTATGCTTTGAGTACTAGGGGTCAAGGAACCTCAGTACCGGTCC 711
Db 667 GAACGAATCTTTTACTATGATGATGATGAGTATGGGGTCAAGGAACCTCAGTACCGGTCC 726
Qy 712 TCA 714
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Db 727 TAA 729

RESULT 7
5455030-16
Patent No. 5455030
APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
POLYPEPTIDE BINDING MOLECULES
NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/40,440
FILING DATE: 1-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 512,910
FILING DATE: 25-APR-1990
APPLICATION NUMBER: 299,617
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 92,110
FILING DATE: 02-SEP-1987
APPLICATION NUMBER: 902,971
FILING DATE: 01-SEP-1986
SEQ ID NO: 16
LENGTH: 729
5455030-16

Query Match      57.2%; Score 408.2; DB 6; Length 729;
Best Local Similarity 75.8%; Pred. No. 6.9e-115;
Matches 548; Conservative 0; Mismatches 163; Indels 12; Gaps 3;

Qy 4 ATTGATGACCCAGACTCCCAATTCTGCTGTATGACGAGAGAGGTTACCAT 63
Db 7 AATGTCACCCAGCTCTCCAGCATATGTCGATCTCCAGGGGAAAGATCACATG 66
Qy 64 ACCTGCAAGGCGAGTCAGATGTGAGT---AATGATGTGCTGGTACCAAGAACCA 120
Db 67 ACCTGCAAGGCGAGTCAGATGTGAGT---AATGATGTGCTGGTACCAAGAACCA 126
Qy 121 GGGCAGTCTCCGAAACTGCTGATATCTCTGATCAATCCGTACACTGAGTCCGTGAT 180
Db 127 GGTGCTCTCCGAAACTGCTGATATCTCTGATCAATCCGTACACTGAGTCCGTGAT 186
Qy 181 CGCTTACCTGGCAGTGTATGGGACGAGTTTCACTTTCACATCAGACATGTCAGAGCT 240
Db 187 CGCTTACCTGGCAGTGTATGGGACGAGTTTCACTTTCACATCAGACATGTCAGAGCT 246
Qy 241 GAAGACCTGGCAGTGTATGGGACGAGTTTCACTTTCACATCAGACATGTCAGAGCT 294
Db 247 GAAGACCTGGCAGTGTATGGGACGAGTTTCACTTTCACATCAGACATGTCAGAGCT 306
Qy 295 ACCAAGCTGGAATTAAGATGAGAGCGGTTCAAGCGAGGTGCTGCGGCGGGA 354
Db 307 CCCAAGCTGGAATTAAGATGAGAGCGGTTCAAGCGAGGTGCTGCGGCGGGA 366
Qy 355 TCGCAGGTGCAAGTGAAGAGTCAAGAGCTGCGGCGGCGGCGGCGGCGGCGG 414
Db 367 CTGATGTGCAAGTGAAGAGTCAAGAGCTGCGGCGGCGGCGGCGGCGGCGG 426
Qy 415 ATCACTGCACTGCTCTGGGTTTTCATTAAACAATTAATGATGATCACTGGGTTGCGCAG 474
Db 427 ATCACTGCACTGCTCTGGGTTTTCATTAAACAATTAATGATGATCACTGGGTTGCGCAG 486
Qy 475 CCTCAGAGAAAGGCTCGAGTGTGAGAGTGAATATGAGTGTGAGAGCAAAATAT 534
Db 487 CCTCAGAGAAAGGCTCGAGTGTGAGAGTGAATATGAGTGTGAGAGCAAAATAT 546
Qy 535 AATTCGGCTCTTATGTCCAGACTGAGATCAAGCAAGCAACTCCAAAGCAAGTTTC 594
Db 547 AATTCGGCTCTTATGTCCAGACTGAGATCAAGCAAGCAACTCCAAAGCAAGTTTC 606
Qy 595 TTAATAATGACAGTCTGCAAACTGATGACACAGCAGTACTACTGTCGA---GTGCG 651
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Db 607 TTAATAATGAACAGTCTGCAAAATTGATGACACAGCCATATCTACTGTGCCAAACGACTG 666

QY 652 GGGGGTAACTACGGCTATGCTTGGACTACTGGGGTAAAGAACTCTAGACCGCTTCC 711

Db 667 GAACGAATCTTTATATAGTACTGACTATTTGGGTCAGAACTCTGACCGCTTCC 726

QY 712 TCA 714

Db 727 TAA 729

RESULT 8

US-08-756-416-38

; Sequence 38, Application US/08756416

; Patent No. 6699715

; GENERAL INFORMATION:

; APPLICANT: Ledbetter, Jeffrey A.

; APPLICANT: Hayden, Martha

; APPLICANT: Fell, Perry

; APPLICANT: Mittler, Robert

; APPLICANT: Winberg, Gosta

; TITLE OF INVENTION: MODIFIED SPY MOLECULES WHICH

; TITLE OF INVENTION: MEDIANE ADHESION BETWEEN CELLS AND USBS

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Merchant & Gould

; STREET: 11150 Santa Monica, Suite 400

; CITY: Los Angeles

; STATE: CA

; COUNTRY: USA

; ZIP: 90025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/756,416

; FILING DATE: 27-NOV-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/007,755

; FILING DATE: 30-NOV-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Adriano, Sarah B

; REGISTRATION NUMBER: 34,470

; REFERENCE/DOCKET NUMBER: 30436.41US01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 310-445-1140

; TELEFAX: 310-445-9031

; TELEX:

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 824 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: Other

; FEATURE:

; US-08-756-416-38

Query Match 56.1%; Score 400.2; DB 4; Length 824;

Best Local Similarity 76.4%; Pred. No. 2.1e-112;

Matches 572; Conservative 0; Mismatches 138; Indels 39; Gaps 5;

QY 4 ATTGTGATGACCAAGTCCCAAAATTCCTGCTATACACAGAGACAGGTTTACATA 63

Db 70 ATTGTGCTACCAATCTCCAGCTCTTTGGCTGTCTCTTAGGAGAGACCAATC 129

QY 64 ACCTGCAAGCCAGTCAAGTGTGAGTAATGATGTGCT-----TGTACCA 111

Db 130 TCTGTCAGAGCCAGTGAAGTGTGTAATATATATGTCACAGTTTAATGACGTGTACAG 189

QY 112 CAGAGCCAGGGCAGTCTCCGAACCTGTGATATACTTGCATCCAAATCGCTACCTGGA 171

Db 190 CAGAGCCAGAGACAGCCACCTCAACTCTTCATCTTTGCTGCATCCAAAGATCTGG 249

QY 172 GTCCCTGATCGCTTCACTGCGAGTGAATAGGACGGAATTTCACTTCCATCAGACT 231

Db 250 GTCCCTGCAAGTTTATGTCAGTGGTCTGGGACAAACTGAGCTCAACATCCATCT 309

QY 232 GTGCAAGCTGAAGACTGGCAGTTTATTTCTGTCACT-----AGATTATAGCTG 282

Db 310 GTGACAGAGATGATGTTGCAATGTATTTCTGTGCAAGAAAGATTCCTTCAAG 369

QY 283 CTCGAGGGGGGACCAAGCTGGAATAA-----GTGAGAGCGGTTTCAAGCGGA 333

Db 370 TTCGAGGGGGGACCAAGCTGGAATAAAGGAGCTTCGGGTGGTGGTCTTGAAGT 429

QY 334 GGTGCTCTGCGCGTGGCGGATCG-----CAGTGCAGGTGAAGAGTCAAGACCTGCG 387

Db 430 GGGGTTCAAGGGCGGCGGTGATCCCTGCTCAGGTGCACTGAAGAGTCAAGACCTGCG 489

QY 388 CTGCTGCGGCTCTCAAGAGCTGTGCTATCACTTGCATCTGTCTTGGGTTTTCATTAC 447

Db 490 CTGCTACCGCCTCAAGAGCTGTGCTATCACTTGTGATCTGTCTGGGTTTTCATTAC 549

QY 448 AATTATGATGATCACTGGGTGGCGCAGCTCCAGAGAAAGTGTGAGTGGCTGGAGTA 507

Db 550 GACTATGATGATCTATTTGGGTGGCGCAGCTCCAGAGAGAGTGAAGTGGCTGGAGTA 609

QY 508 ATATGGCTGTGAGAGCAAAATTAATTCGCTTTATGTCCAGACTGAGCATCAGC 567

Db 610 ATATGGCTGTGAGAGCAAAATTAATTCGCTTTATGTCCAGACTGAGCATCAGC 669

QY 568 AAGGACACTCCAGAGCCAGTTTCTTAAATTAAGTGTGCAAACTGATGACCA 627

Db 670 AAGGACACTCCAGAGCCAGTTTCTTAAATTAAGTGTGCAAACTGATGACCA 729

QY 628 GCCATGTACTACGTGTCAG-----TGCGGGGGGTAATAAGGCTGATGCTTGGACTGCG 684

Db 730 GCCGTATTAATCTGTGTCAGAGTAAGGATTAAGGATTAAGGATTAAGGATTAAG 789

QY 685 GGTCAAGAACTCACTCACTCCGCTCTCTC 713

Db 790 GGTCAAGAACTCACTCACTCCGCTCTCTC 818

RESULT 9

US-08-860-174A-1

; Sequence 1, Application US/08860174A

; Patent No. 5989830

; GENERAL INFORMATION:

; APPLICANT: DAVIS, Paul James

; APPLICANT: VAN DER LOGT, Cornelis Paul Erik

; APPLICANT: VERHOEIJEN, Martine Elisa

; APPLICANT: WILSON, Steve

; TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT

; TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP

; STREET: 1100 New York Avenue, N.W.

; CITY: WASHINGTON, D.C.

; STATE:

; COUNTRY: UNITED STATES

; ZIP: 20005-3918

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text

; SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/860,174A

Db 74 ACATGTCGACGAGTGGGAATATTCACAAATTATTGACATGATCAGAGAAACAGGGA 133
QY 124 CAGCTCCGAAACGCTGATATCTCTGCATCCAAATGGCTACACTGAGTCCCTGATCCG 183
Db 134 AAATCTCTCAGCTCCCTGCTCTATATACAAACCTTACAGATGGTGTGCCATCAGG 193
QY 184 TTCACTGGCAGTGATATGGAACGAGATTTCATCTTCCATCAGACTGTGAGAGCTGAA 243
Db 194 TTCACTGGCAGTGATATGGAACCAATATTTCTCTCAAGATCAACAGCCTGCAACCTGA 253
QY 244 GACCTGCGAGTTATTTCTGTCTGACAGAGATT-----ATAGCTGCTGGAGGCGG 294
Db 254 GATTTGGAGATTATCTGTCACAACTTTTGGAGTACTCTCGAGGTTCCGGTGAGGG 313
QY 295 ACCAAGCTGGAATAA---GGTGAGCGGGTTCCAGCCGAGAGTGGCTCTGGCGGTGC 351
Db 314 ACCAAGCTGGAATAAAGCGGGGTGAGCGGGTTCCAGCGAGGTGGCTCTGGCGGTGC 373
QY 352 GGATCGCAGGTGCGAGTGAAGAGTCAAGACCTGGCTGGTGGCGCCCTCAGAGGCTG 411
Db 374 GGATCGCAGGTGCGAGTGAAGAGTCAAGACCTGGCTGGTGGCGCCCTCAGAGGCTG 433
QY 412 TCCATCACTGCACTGTCTGTGGTTTCAATTAACTAATGATGTGATCACTGGGTGCG 471
Db 434 TCCATCACTGCACTGTCTGTGGTTTCAATTAACTAATGATGTGATCACTGGGTGCG 493
QY 472 CAGCTCCAGAAAGGCTGTGAGTGGCTGGAGATATATGGGCTGTGAGAGCAAT 531
Db 494 CAGCTCCAGAAAGGCTGTGAGTGGCTGGAGATATATGGGCTGTGAGAGCAAT 553
QY 532 TATATTCGCTCTTATGTCCAGACTGAGATCAGCAAGGCAACTCCAAAGGCAAGT 591
Db 554 TATATTCGCTCTTATGTCCAGACTGAGATCAGCAAGGCAACTCCAAAGGCAAGT 613
QY 592 TTCTTAAATGAACAGTCTGCAAACTGATGACACAGCCATGTACTAATGCTGCG 651
Db 614 TTCTTAAATGAACAGTCTGCAAACTGATGACACAGCCATGTACTAATGCTGCG 673
QY 652 GGGGTGACATGAGCTATGCTTGTGACTACTGGGGTCAAGAACTGATGACCTGTCC 711
Db 674 AGAGAT-----TATAGCTTGAATCTGGGGCCAAAGGACACAGGTCACTGTCC 724
QY 712 TCA 714
Db 725 TCA 727

RESULT 11
US-08-197-834-6
Sequence 6, Application US/08197834
Patent No. 5639455
GENERAL INFORMATION:
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: NAKAZAWA, HARUMI
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, WAIR & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08197,834

FILING DATE: 514
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 028173/1993
FILING DATE: 17-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5639455man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-661-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: DNA (synthetic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..738
US-08-197-834-6

Query Match 55.5%; Score 396.2; DB 1; Length 738;
Best Local Similarity 75.5%; Pred. No. 3.3e-111;
Matches 55; Conservative 0; Mismatches 153; Indels 27; Gaps 4;

QY 4 ATGTGATGACCCAGATCCCAATTCCTGTTGATCAGAGAGACAGGGTTACCAT 63
Db 7 ATCTGCTGACACAGTCTCAAAATTCCTGTTGATCAGAGAGACAGGGTTACCAT 66
QY 64 ACTCGAAGCCAGTGAAGTGTGATATGATGTGCTTGGTATCCAAAGAACAGG 123
Db 67 ACTCGAAGCCAGTGAAGTGTGATATGATGTGCTTGGTATCCAAAGAACAGG 126
QY 124 CAGTCCGAAACTGCTGATATCTCTGATCCATTCGCTAAGTCTGATCCG 183
Db 127 CAGTCTCTTAATCTGATATCTGATCTGATCCATTCGCTAAGTCTGATCCG 186
QY 184 TTCACTGGCAGTGATATGGAACGATTTCACTTTCACCATCAGACTGTGAGTGA 243
Db 187 TTCACTGGCAGTGATATGGAACGATTTCACTTTCACCATCAGACTGTGAGTGA 246
QY 244 GACCTGCGAGTTATTTCTGTGACAGATTATG-----CTGCTCGAGGGGG 294
Db 247 GACCTGCGAGTTATTTCTGTGACAGATTATG-----CTGCTCGAGGGGG 306
QY 295 ACCAAGCTGGAAATTAAGGTGAGGCGGTTCAAGCGGAGGTGCTGTGGCGGTGCGGA 354
Db 307 ACCAAGCTGGAAATTAAGGTGAGGCGGTTCAAGCGGAGGTGCTGTGGCGGTGCGGA 363
QY 355 TCCAGAGTGCAGTGAAGAGTCAAGACCTGGCTGTGGCGGCTTCAAGAGCTGTGC 414
Db 364 ACCAGAGTCAAACTCGAGAGTCTGGCCTGGGATTTTCAGAGCCTCCAGACCTCA 423
QY 415 ATCACTGCACTGTCTGTGGGTTTCATTAACCAATTAT-----GTGTCACTGGGTT 468
Db 424 CTGACTGTGTTCTTCTCTGGGTTTTCATGAGCACTTCTGTATGAGTGTGAGCTGAT 483
QY 469 CGCAGCCTTCAGAAAGGCTCTGAGGTGGCTGGAGTAAATAGGCTGTGGAACACA 528
Db 484 CGTCACTTCAGAAAGGCTCTGAGGTGGCTGGAGTAAATAGGCTGTGGAACACA 543
QY 529 AATTATATTCGCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTCCAAAGCCAA 588
Db 544 CACTATPACCATTCCTGGAAGCGGCTCACAATCTCCAAAGATACCTCCAAACAG 603
QY 589 GTTTCTTAAATGAACAGTCTGCAAACTGATGACACAGCCATGTAATCTGTGCTAGT 648
Db 604 GTATCTCTCAAGATCAAGTGTGACACTGAGATATGCGCACATATCTTGTGCTCGA 663

QY 649 CG-----GGGGGTTACTAGCGCTATGCTTTGGACTACTAGGGGTCAGAACTCTCA 699
DB 664 AGAAGTCTATGTAATTTGGGGGACTATGACTATGACTAGGGGTCAGAACTCTCA 723
QY 700 GTCAACGCTCTCTCTCA 714
DB 724 GTCAACGCTCTCTCTCA 738

RESULT 12
US-09-742-693-29
Sequence 29, Application US/09742693
Patent No. 6579842
GENERAL INFORMATION:
APPLICANT: HOWELL, Steven
APPLICANT: LITTLE, Julie C.
APPLICANT: VAN DER LOGT, Cornelis P.
APPLICANT: BARRY, Neil J.
TITLE OF INVENTION: METHOD OF TREATING FABRICS
FILE REFERENCE: C7536 (V)
CURRENT APPLICATION NUMBER: US/09/742,693
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: EP9310431.4
PRIOR FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 734
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-742-693-29

Query Match 55.3%; Score 394.8; DB 4; Length 734;
Best Local Similarity 75.0%; Pred. No. 8.8e-111;
Matches 540; Conservative 0; Mismatches 162; Indels 18; Gaps 3;

QY 4 ATTGTGATGACCCAGACTCCCAAAATTCCTGCTGTATGAGCAGAGAGACAGGGTTACATA 63
DB 14 ATCAGAGTCACCCAGTCTCCAGCCTCCTTTCTGGCTGTGGAGAAACGTCAACATC 73
QY 64 ACCTGCAAGGCGAGTCAAGTGTGATGATGCTTGGTGTACCAACAGAGCCAGGG 123
DB 74 ACATGTGAGCAAGTGGGAAATATTCACAAATTTAGCATGTATCAGCAAAACAGGGA 133
QY 124 CAGCTCCGAAACGCTGATATATCTGTCATCCAAATGCTACGTCAGTGGAGTCCCTGATGC 183
DB 134 AAATCTCTCAGCTCTGCTGTATATTAACAACAACCTTACAGATGAGTGTGCTCAAGG 193
QY 184 TTCACTGAGATGATATGAGACGAGATTTCATTTACCATCAGACTGTGACAGGCTGAA 243
DB 194 TTCACTGAGATGATATGAGACGAGATTTCATTTACCATCAGACTGTGACAGGCTGAA 253
QY 244 GACCTGCAAGTTATTTCTGTCAGAGGATTAAGCTGCTGG-----AGGGGGAGCC 297
DB 254 GATTTTGGAGTTATTTCTGTCAGAGGATTAAGCTGCTGG-----AGGGGGAGCC 313
QY 298 AAGCTGGAATATAA---GGTGAAGGGGTTCAAGCGAGGAGTGGCTGGGGGTGGGCGGA 354
DB 314 AAGCTCGAGATCAACCGGGGAGGAGGCGGTTCAAGCGAGGAGTGGCTGGGGGTGGGCGGA 373
QY 355 TCGCAGGTGACAGTGAAGAGTCAAGACTGAGCTGAGTGGCGCCCTCAAGAGCTGTCC 414
DB 374 TCGCAGGTGACAGTGAAGAGTCAAGACTGAGCTGAGTGGCGCCCTCAAGAGCTGTCC 433
QY 415 ATCACTTGCATGTCTCTGGGTTTTCATTAACCAATTAATGTTGACACTGGGTTGCCAG 474
DB 434 ATCACTTGCATGTCTCTGGGTTTTCATTAACCAATTAATGTTGACACTGGGTTGCCAG 493
QY 475 CCTCAGAGAAAGGCTGAGTGGCTGGAGTAATATGAGGCTGGGTCAGAGCAAAATTA 534

DB 494 CCTCAGAGAAAGGCTGAGTGGCTGGAGTAATTTGGGGTATGAAACACAGACTAT 553
QY 535 AATTCGGCTCTTATGTCCAGACTGAGCATCAAGCAAGCAACTCAAGAGCAAGTTTC 594
DB 554 AATTCAGCTCTCAAAATCAGACTGAGCATCAAGCAAGCAACTCAAGAGCAAGTTTC 613
QY 595 TTAATAATGAACAGTGCAGAACTGATGACACAGCCATGTACTAGTGGCAGTGGGGG 654
DB 614 TTAATAATGAACAGTGCAGAACTGATGACACAGCCAGTACTAGTGGCAGAGAGA 673
QY 655 GGTAACTACGCTATGCTTTGACTACTGAGGCTCAAGAACTTCAGTCACTGCTCTCA 714
DB 674 GAT-----TATAGCTTGACTAGTGGGGCCAAAGAGACAGGTCACTCTCTCA 724

RESULT 13
5455030-14
Patent No. 5455030
APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
POLYPEPTIDE BINDING MOLECULES
NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/40,440
FILING DATE: 1-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 512,910
FILING DATE: 25-APR-1990
APPLICATION NUMBER: 299,617
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 92,110
FILING DATE: 02-SEP-1987
APPLICATION NUMBER: 902,971
FILING DATE: 01-SEP-1986
SEQ ID NO:14
LENGTH: 720
5455030-14

Query Match 55.1%; Score 393.6; DB 6; Length 720;
Best Local Similarity 75.8%; Pred. No. 2e-110;
Matches 550; Conservative 0; Mismatches 149; Indels 27; Gaps 4;

QY 4 ATTGTGATGACCCAGACTCCCAAAATTCCTGCTGTATGAGCAGAGAGACAGGGTTACATA 63
DB 7 AATGTGTCACCCAGTCTCCAGCATATGCTGCACTCTCCAGGAAAGTCAACATG 66
QY 64 ACCTGCAAGGCGAGTCAAGTGTGAGT---AATGATGTGCTTGGTGTACCAACAGAGCCA 120
DB 67 ACCTGCAAGGCGAGTCAAGTGTGAGT---AATGATGTGCTTGGTGTACCAACAGAGCCA 126
QY 121 GGGCAGTCTCCGAAACGCTGATATATCTGTCATCCAAATGCTACACTGAGTCCCTGAT 180
DB 127 GGTGCTCTCCGAAACGCTGATATATCTGTCATCCAAATGCTACACTGAGTCCCTGAT 186
QY 181 CGCTTCACTGAGCATGATATGAGACGAGATTTCATTTCACTTCAACATCAGACTGTGCAAGCT 240
DB 187 CGCTTCACTGAGCATGATATGAGACGAGATTTCATTTCACTTCAACATCAGACTGTGCAAGCT 246
QY 241 GAAGACCTGACAGTTATTTCTGTCAGAGGATTAAG-----CTGCTCGAGAGG 291
DB 247 GAAGACCTGACAGTTATTTCTGTCAGAGGATTAAG-----CTGCTCGAGAGG 306
QY 292 GGGACCAAGCTGGAATATAAAGTGAAGCGGTTCAAGCGAGAGTGGCTCTGGCGGTGGC 351
DB 307 GGGACCAAGCTGGAATATAAAGTGAAGCGGTTCAAGCGAGAGTGGCTCTGGCGGTGGC 354
QY 352 GGAATCGAGGTGAGAGTGAAGAGTCAAGACTGAGCTGAGTGGCGCCCTCAAGAGCTGT 411
DB 355 TCTAATCTACTCACTGAGAGAGTCAAGACTGAGCTGAGTGGCGCCCTCAAGAGCTGT 414
QY 412 TCCATCACTTGCATGTCTCTGGGTTTTCATTAACCAATTAATGTTGACACTGGGTTGCC 471
DB 415 TCCATCACTTGCATGTCTCTGGGTTTTCATTAACCAATTAATGTTGACACTGGGTTGCC 474

QY 472 CAGCTTCAGAGAAAGGCTGAGTGGCTGGAGTATATAGGCTGTGAGACAAAT 531
| | | | |
Db 475 CAGCTTCAGAGAAAGGCTGAGTGGCTGGAGTATATAGGCTGTGAGACAAAT 534
| | | | |
QY 532 TATTAATTCAGCTCTTATATGTCGAGCTGAGCATCAGAGAGCAATTCAGAGCAAGTT 591
| | | | |
Db 535 TATTAATTCAGCTCTTATATGTCGAGCTGAGCATCAGAGAGCAATTCAGAGCAAGTT 594
| | | | |
QY 592 TTCTTAAATGAACAGCTGCAAACTGATGACACAGCCCATGTACTAGTGGCA---GT 648
| | | | |
Db 595 TTCTTAAATGAACAGCTGCAAAATGATGACACAGCCCATGTACTAGTGGCAAGCA 654
| | | | |
QY 649 CGGGGGGTAACGCTATGCTTGGAGTCTGAGGCTCAGAGAACTCAGTCAACCTG 708
| | | | |
Db 655 CTGGAACGAAATGTTTACTATGCTATGAGACTATTGGGGTCAAGGAACCTCAGTCAACCTG 714
| | | | |
QY 709 TCCTCA 714
| | | | |
Db 715 TCCTAA 720
| | | | |

RESULT 14
5455030-14
; Patent No. 5455030
; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO: 14:
; LENGTH: 720
5455030-14

Query Match 55.1%; Score 393.6; DB 6; Length 720;
Best Local Similarity 75.8%; Pred. No. 2e-110; Indels 27; Gaps 4;
Matches 550; Conservative 0; Mismatches 149;

QY 4 ATTGTGATGACCCAGACTCCCAAAATTCCTGCTGTATCAGCAGAGAGACAGGGTTACCAT 63
| | | | |
Db 7 AATGTGCTCACCCAGCTCTCAGAGCATATGTCGATCTCAGAGGAGAAAGTCCACATG 66
| | | | |
QY 64 ACCTGCAAGCCAGCTCAGAGTGAAGT---AATGATGCTGCTGTGATCCAAAGAACCA 120
| | | | |
Db 67 ACCTGCAAGCCAGCTCAGAGTGAAGTTCAGATTAATTCACATCTTCCAGCAGAGAGTCA 126
| | | | |
QY 121 GGGGAGCTCCGAAAGCTGATATATCTGCAATCCAAATGGCTACATGAGAGTCCCAT 180
| | | | |
Db 127 GGGGCTCCCAAACTCTGGGTTATGAGCAATCCAACTTGGTTGAGAGTCCCAT 186
| | | | |
QY 181 CGCTTCACTGGCAGTGAATAGGACGGAATTTTCATTTCAACATCAGACACTGTCAGAGCT 240
| | | | |
Db 187 CGCTTCACTGGCAGTGAATAGGACGGAATTTTCATTTCAACATCAGACACTGTCAGAGCT 246
| | | | |
QY 241 GAAGACTGCGAGTTATTTCTGTGACAGAGATTATG-----CTGCTGGAGGG 291
| | | | |
Db 247 GAAGACTGCGAGTTATTTCTGTGACAGAGATTATG-----CTGCTGGAGGG 306
| | | | |
QY 292 GGGACCAAGCTGGAATAAAGAGTGAAGCGGCTTCAAGCGGAGAGTGGCTCTGGCGGGTGC 351
| | | | |
Db 307 GGGACCAAGCTGGAAGTGAAGGTTAA-----TCTTCTGGTCTGGTTCCGAA 354
| | | | |

QY 352 GGATCGCAGAGTGCAGGTGAAGAGTCAAGACCTGGCTGTGGCCGCTCAGAGAGCTTG 411
| | | | |
Db 355 TCTAATTTACTACAGCTGAAGAGTCAAGACCTGGCTGTGGCCGCTCAGAGAGCTTG 414
| | | | |
QY 412 TCCATCACTTGCAGCTCTCTGGGTTTTTCAATTAACCAATTATGATGTATCACTGGTTCCG 471
| | | | |
Db 415 TCCATCACTTGCAGCTCTCTGGGTTTTTCAATTAACCAATTATGATGTATCACTGGTTCCG 474
| | | | |
QY 472 CAGCTTCAGAGAAAGGCTGAGTGGCTGGAGTATATAGGCTGTGAGACAAAT 531
| | | | |
Db 475 CAGCTTCAGAGAAAGGCTGAGTGGCTGGAGTATATAGGCTGTGAGACAAAT 534
| | | | |
QY 532 TATTAATTCAGCTCTTATATGTCGAGCTGAGCATCAGAGAGCAATTCAGAGCAAGTT 591
| | | | |
Db 535 TATTAATTCAGCTCTTATATGTCGAGCTGAGCATCAGAGAGCAATTCAGAGCAAGTT 594
| | | | |
QY 592 TTCTTAAATGAACAGCTGCAAACTGATGACACAGCCCATGTACTAGTGGCA---GT 648
| | | | |
Db 595 TTCTTAAATGAACAGCTGCAAAATGATGACACAGCCCATGTACTAGTGGCAAGCA 654
| | | | |
QY 649 CGGGGGGTAACGCTATGCTTGGAGTCTGAGGCTCAGAGAACTCAGTCAACCTG 708
| | | | |
Db 655 CTGGAACGAAATGTTTACTATGCTATGAGACTATTGGGGTCAAGGAACCTCAGTCAACCTG 714
| | | | |
QY 709 TCCTCA 714
| | | | |
Db 715 TCCTAA 720
| | | | |

RESULT 15
US-09-554-765-12
; Sequence 12, Application US/09554765
; Patent No. 6551495
; GENERAL INFORMATION:
; APPLICANT: Porter, Robert A
; APPLICANT: Badley, Robert A
; TITLE OF INVENTION: Electroactive Surfaces
; FILE REFERENCE: IMIN.P-036
; CURRENT APPLICATION NUMBER: US/09/554,765
; CURRENT FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: PCT/GB98/03495
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 739
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: bispecific scFv4155-HCV3 and HCV24 construct
US-09-554-765-12

Query Match 55.1%; Score 393.2; DB 4; Length 739;
Best Local Similarity 74.9%; Pred. No. 2.7e-110; Indels 18; Gaps 3;
Matches 539; Conservative 0; Mismatches 163;

QY 4 ATTGTGATGACCCAGACTCCCAAAATTCCTGCTGTATCAGCAGAGAGACAGGGTTACCAT 63
| | | | |
Db 14 ATGAGACTCACCCAGCTCTCAGAGCTCTCTTTCTGGCTGTGGAGAAACTGTACACATC 73
| | | | |
QY 64 ACCTGCAAGCCAGTCAAGAGTGAAGTGAATGATGTTGGCTTGTACCAAGAACCAAGG 123
| | | | |
Db 74 ACATGTCGAGCAAGTGGGAATATTCACATTTATTTGATGATGATCAGAGAGAAACAGGG 133
| | | | |
QY 124 CAGTCTCCGAAACTGTGATATATCTGATGATCAATTCGCTACACTGGAATCCTGATCGC 183
| | | | |
Db 134 AATATCTCTCAAGCTCTGCTGATATATTAACAACAACTTGAAGATGATGATGATCAAGG 193
| | | | |
QY 184 TTCACTGGAGTGAATAGGAGACGGAATTTCACTTCAACATCAGACTGTGCGAGCTGAA 243
| | | | |
Db 194 TTCACTGGAGTGAATAGGAGACGGAATTTCTCTTAAGATCAACAGCTGTCAACTGAA 253
| | | | |
QY 244 GACCTGCGAGTTATTTCTGTGACGAGATTAATAGCTCGCTGG-----AGGGGGAGCC 297
| | | | |

```

Db      254 GATTTTGGAGATTATTACTGTCAACATTTTGGAGTACTCCTCGAGCCTTCGGTGGAAAC 313
Qy      298 AAGCTGGAATATAA---GATGAGGCGGTTCAAGCGAGGTGGCTCTGGCGGTGGCGGA 354
Db      314 AAGCTCGAGATCAAAAGGGGTGGAGCGGTTCAAGCGAGGTGGCTCTGGCGGTGGCGGA 373
Qy      355 TCGCAGGTGCAAGGTGAAGAGTCAAGACCTGGCTGGTGGCGGCTTCAGAGCCTGTCC 414
Db      374 TCGCAGGTGCAAGGTGCAAGAGTCAAGACCTGGCTGGTGGCGGCTTCAGAGCCTGTCC 433
Qy      415 ATCACTTGCACTGTCTGTGGGTTTCATTAAACAATTATGGTGTACACTGGGTTGCCAG 474
Db      434 ATCAATGCAACGCTCTCAGGTTCTCATTAACCGGCTATGGTGAACCTGGGTTGCCAG 493
Qy      475 CCTCCAGGAAAGGCTGTGAGTGGCTGGAGTAATATGGGCTGTGGAAGCAAAATTAT 534
Db      494 CCTCCAGGAAAGGCTGTGAGTGGCTGGAGTAATATGGGCTGTGGAAGCAAAATTAT 553
Qy      535 AATTGGGCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTCCAGAGCCAAATTTC 594
Db      554 AATTGAGCTCTCAATCCAGACTGAGCATCAGCAAGCAAACTCCAGAGCCAAATTTC 613
Qy      595 TTAAATAATGACAGTCTGCAATGATGACAAGCCATGTACTGTGCCAGTGGGG 654
Db      614 TTAAATAATGACAGTCTGCAATGATGACAAGCCAGTACTGTGCCAGAGAGA 673
Qy      655 GGTAACTACGGCTATGCTTTGAGTACTGGGGTCAAGGAACCTCAGTACCGCTCTCTCA 714
Db      674 GAT-----TATAGGCTTGACTACTGGGGCGAAGGCACACGGGTCAACCGTCTCTCA 724

```

Search completed: February 18, 2005, 23:56:50
 Job time : 151.69 secs

OY	6	ATAACCTGCAAGGCGAGTCAAGTGTGAGTAATGAATGAGGCTTGGTACCAACAGAAAGCA	122
Db	61	ATAACCTGCAAGGCGAGTCAAGTGTGAGTAATGAATGAGGCTTGGTACCAACAGAAAGCA	122
OY	121	GAGGCACTTCGCGAAACTGCTGATATATCTGTGATCCAAATCGCTACATCACTGAGTCCGTAT	180
Db	121	GAGGCACTTCGCGAAACTGCTGATATATCTGTGATCCAAATCGCTACATCACTGAGTCCGTAT	180
OY	181	CGCTTCACTGGCAGTGTGATATGGAACGGAATTTCACTTTTCAACCATATGAGCATGTGAGAGCT	240
Db	181	CGCTTCACTGGCAGTGTGATATGGAACGGAATTTCACTTTTCAACCATATGAGCATGTGAGAGCT	240
OY	241	GAAGACCTGGCAGTATTTATTTCTGTACAGAGATTAATAGCTGCTCGGAGGGGGGAGCAAG	300
Db	241	GAAGACCTGGCAGTATTTATTTCTGTACAGAGATTAATAGCTGCTCGGAGGGGGGAGCAAG	300
OY	301	CTGGAAATTAAGGTGAGAGCGGTTTCAGGCGAGAGGTGCTCTGCGGTGCGGATTCGAG	360
Db	301	CTGGAAATTAAGGTGAGAGCGGTTTCAGGCGAGAGGTGCTCTGCGGTGCGGATTCGAG	360
OY	361	GTGCAAGTGAAGAGATCAGAGCTTGCGCTGTGCGGCTTCAAGAGCTGTGCATCACT	420
Db	361	GTGCAAGTGAAGAGATCAGAGCTTGCGCTGTGCGGCTTCAAGAGCTGTGCATCACT	420
OY	421	TGCACGTCTCTGGGTTTTTCAATTAACAATTATNGGTATACCTGGGTTTCGCGAACCTTCA	480
Db	421	TGCACGTCTCTGGGTTTTTCAATTAACAATTATNGGTATACCTGGGTTTCGCGAACCTTCA	480
OY	481	GGAAGAGGTCTGAGAGTGTGCGGAGATATATGAGGCTGTGGAGAGCAAAATTAATATTCG	540
Db	481	GGAAGAGGTCTGAGAGTGTGCGGAGATATATGAGGCTGTGGAGAGCAAAATTAATATTCG	540
OY	541	GCTCTTATGTCCAGACTGAGCATCAGCAAGACAACTCCAAAGGCGAAATTTTCTTAAA	600
Db	541	GCTCTTATGTCCAGACTGAGCATCAGCAAGACAACTCCAAAGGCGAAATTTTCTTAAA	600
OY	601	ATGAACAGTGTGAACTGATATGACACAGCATGTACTCTGTGCCAGTGTGGGGGGGTATAC	660
Db	601	ATGAACAGTGTGAACTGATATGACACAGCATGTACTCTGTGCCAGTGTGGGGGGGTATAC	660
OY	661	TACGGCTATCTTTGGACTACTGAGGGTCAAGGAACCTCAGTCAACCGTCTCTCA	714
Db	661	TACGGCTATCTTTGGACTACTGAGGGTCAAGGAACCTCAGTCAACCGTCTCTCA	714
RESULT 2			
US-10-075-947A-2			
: Sequence 2, Application US/10075947A			
: Publication No. US20030147808A1			
GENERAL INFORMATION:			
APPLICANT: Cheung, Nai-Kong V.			
APPLICANT: Larson, Steven M.			
APPLICANT: Guo, Hong-Pen			
APPLICANT: Rivlin, Ken			
APPLICANT: Sadelain, Michel			
TITLE OF INVENTION: Single Chain FV Constructs of Anti-Ganglioside GD2			
FILE REFERENCE: MSK-P-013-2			
CURRENT APPLICATION NUMBER: US/10/075,947A			
CURRENT FILING DATE: 2002-02-13			
PRIOR APPLICATION NUMBER: 09/142,974			
PRIOR FILING DATE: 1998-09-18			
PRIOR APPLICATION NUMBER: PCT/US97/04427			
PRIOR FILING DATE: 1997-03-20			
PRIOR APPLICATION NUMBER: 60/103,703			
PRIOR FILING DATE: 1996-03-20			
NUMBER OF SEQ ID NOS: 5			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 2			
LENGTH: 714			
TYPE: DNA			
ORGANISM: Murine			
FEATURE:			

OTHER INFORMATION: 3G6-BCFV									
US-10-075-947A-2									
Query Match	Similarity	100.0%;	Score 714;	DB 15;	Length 714;				
Best Local	Similarity	100.0%;	Pred. No. 8.8e-216;						
Matches	714;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	AGATTTGATGATGACCCAGACTCTCCCAATTTCTGCTTGATATAGACAGAGAAAGGGTTTACC	60						
Db	1	AGATTGTGATGATGACCCAGACTCTCCCAATTTCTGCTTGATATAGACAGAGAAAGGGTTTACC	60						
QY	61	ATAACCTGCAGAGGCGAGTCAAGAGTGTAGTAAATGATGATGGCTTGATACAGAGCAAGAGCCA	120						
Db	61	ATAACCTGCAGAGGCGAGTCAAGAGTGTAGTAAATGATGATGGCTTGATACAGAGCAAGAGCCA	120						
QY	121	GGGCGAGTCTCCGAAACTGCTGATATACTCTTGATCCAAATGCTTACACTGAGTCCCTGAT	180						
Db	121	GGGCGAGTCTCCGAAACTGCTGATATACTCTTGATCCAAATGCTTACACTGAGTCCCTGAT	180						
QY	181	CGCTTCACTGGCAGATGATATGGACGGATTTCACTTTACATCAGACACTGTGACAGCT	240						
Db	181	CGCTTCACTGGCAGATGATATGGACGGATTTCACTTTACATCAGACACTGTGACAGCT	240						
QY	241	GAAGACCTGGAGATTATTTCTGTACAGAGGATTAATGCTGCTGGAGGGGGGAGACCAAG	300						
Db	241	GAAGACCTGGAGATTATTTCTGTACAGAGGATTAATGCTGCTGGAGGGGGGAGACCAAG	300						
QY	301	CTGGAAATTAAGAGGTGAGGCGGTTTCAGGCGGAGAGTGGCTCTGGCGGTGCGGATTCGACG	360						
Db	301	CTGGAAATTAAGAGGTGAGGCGGTTTCAGGCGGAGAGTGGCTCTGGCGGTGCGGATTCGACG	360						
QY	361	GTCGAGGTGAAGAGTCAAGACTCTGGCTGTGGTGGCGCTTCACAGAGCTGTTCATCACT	420						
Db	361	GTCGAGGTGAAGAGTCAAGACTCTGGCTGTGGTGGCGCTTCACAGAGCTGTTCATCACT	420						
QY	421	TGCACTGTCTCTGGGTTTTCATTAACCAATTATGTGTATCACTGGGTTTGGCAGCTTCCA	480						
Db	421	TGCACTGTCTCTGGGTTTTCATTAACCAATTATGTGTATCACTGGGTTTGGCAGCTTCCA	480						
QY	481	GGAAGGGGTCTGAGTGGCTGGGAGTAAATATGGGCTGTGGAGACACAATAATTAAATTGCG	540						
Db	481	GGAAGGGGTCTGAGTGGCTGGGAGTAAATATGGGCTGTGGAGACACAATAATTAAATTGCG	540						
QY	541	GCTCTTATATGTCACAGACTGAGCATCAGACAGGACAACTTCCAAAGGCCAAAGTTTCTTAAAA	600						
Db	541	GCTCTTATATGTCACAGACTGAGCATCAGACAGGACAACTTCCAAAGGCCAAAGTTTCTTAAAA	600						
QY	601	ATGAACAGTCTGCAAACTGATGACACAGGCAATGACTACTGTGCAGTCCGGGGGGGTAC	660						
Db	601	ATGAACAGTCTGCAAACTGATGACACAGGCAATGACTACTGTGTGCAAGTCCGGGGGGGTAC	660						
QY	661	TACGGCTATGCTTTGGACTACTGCGGGGTCAAGAAACTCAGTCAACGCTCTCTCA	714						
Db	661	TACGGCTATGCTTTGGACTACTGCGGGGTCAAGAAACTCAGTCAACGCTCTCTCA	714						
RESULT 3									
US-10-075-947A-4									
Sequence 4, Application US/10075947A									
Publication No. US20030147808A1									
GENERAL INFORMATION:									
APPLICANT: Cheung, Nai-Kong V.									
APPLICANT: Larson, Steven M.									
APPLICANT: Guo, Hong-Fen									
APPLICANT: Raylin, Ken									
APPLICANT: Sadelain, Michel									
TITLE OF INVENTION: Single Chain FV Constructs of Anti-Ganglioside GD2									
FILE REFERENCE: MSK_P-013-2									
CURRENT APPLICATION NUMBER: US/10/075,947A									
PRIORITY FILING DATE: 2002-02-13									
PRIORITY FILING DATE: 09/142,974									
PRIORITY FILING DATE: 1998-09-18									

Query Match	67.2%	Score 480	DB 18	Length 1479
Best Local Similarity	81.5%	Pred. No. 2.1e-141		
Matches 587	Conservative	0	Mismatches 115	Indels 18
				Gaps 2

Db 662 -----AGAACTGTCGTTGCTTACTGGGCCAAGGACCAACGGTCAACCGTCTCCTC 713

OTHER INFORMATION: scFv EpcamxCD3 with M4 mutant in anti-CD3 part
US-10-682-845-64

Db 603 CTTTAAATGACACAGTCTGCAAGCTAATGACACAGCCATATATTACTGTGCCAGATGC- 661

Qy 654 GGGTAACGAGGCTATGCTTTGAGTACTAGGGGTCAGAGAACTTCAGTCAACCGTCTCTC 713
Db 662 -----AGAACTGCTGTTTGCTTACTGAGGCGCAAGGAGCAACGGTCAACCGTCTCTC 713

RESULT 7

US-10-682-845-66
; Sequence 66, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: LanzaVecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAMCD3 with M7 mutant in anti-CD3 part
US-10-682-845-66

Query Match 67.2%; Score 480; DB 18; Length 1479;
Best Local Similarity 81.5%; Pred. No. 2,1e-141;
Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

Qy 3 TATTGTATGATGACCCAGACTCCCAATTCTGCTGTATACAGCAGAGACAGGGTTACCAT 62
Db 3 TATCCAGGTGACCCAGTCTCAAAAATTCATGTCACATCAATAGAGAGACAGGGTCAGCGT 62
Qy 63 AACCTGCAAGGCCAGTCAAGTGTGATGATGATGTGGCTTGTGACCAACGAAAGCCAGG 122
Db 63 CACCTGCAAGGCCAGTCAAGTGTGATGATGATGTGGCTTGTGACCAACGAAAGCCAGG 122
Qy 123 GCAATCTCTTAAGACATGATTTACTCGGCATCTTACCGGTACAGTGGAGTCCCTGATCG 182
Db 123 GCAATCTCTTAAGACATGATTTACTCGGCATCTTACCGGTACAGTGGAGTCCCTGATCG 182
Qy 183 CTTCACTGCAAGTGGATATGAGAGCGAATTTCACTTTCACATCAGCACTGTGACAGCTGA 242
Db 183 CTTCACTGCAAGTGGATATGAGAGCGAATTTCACTTTCACATCAGCACTGTGACAGCTGA 242
Qy 243 AGACCTGGCACTTATTTCTGTCTGACAGAGATTATAGCT-----CGCTCGAAGGGG 293
Db 243 AGACCTGGCAAGATTATTTCTGTCTGACAGATTATAGCT-----CGCTCGAAGGGG 293
Qy 294 GACCAAGCTGGAATTAAGAGTGAAGCGGTTCACGCGGAGAGTGGCTTCGCGGTGCGG 353
Db 303 GACCAAGCTGGAATTAAGAGTGAAGCGGTTCACGCGGAGAGTGGCTTCGCGGTGCGG 353
Qy 354 ATGCAAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 413
Db 363 TTCTCAGGTGAATCTGACAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGT 422
Qy 414 CATCACTTGAAGTCTGCTGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 473
Db 423 CATCACTTGAAGTCTGCTGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 482
Qy 474 GCTTCGAGAAAGGCTCTGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 533
Db 483 GCTTCGAGAAAGGCTCTGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 542
Qy 534 TAAATTCGAGCTTATATGTCAGATGAGCATGAGCAAGCAACTTCAAGAGCCAAAGTTT 593
Db 543 TAAATTCGAGCTTATATGTCAGATGAGCATGAGCAAGCAACTTCAAGAGCCAAAGTTT 602

Qy 594 CTTAAATATGAAAGTCTGCAAACTGATGACAGAGCCATGACTACTGTGCGAGTGGGG 653
Db 603 CTTAAATATGAAAGTCTGCAAACTGATGACAGAGCCATATATTATGTCGCAAAATGG- 661
Qy 654 GGGTAACGAGGCTATGCTTTGAGTACTAGGGGTCAGAGAACTTCAGTCAACCGTCTCTC 713
Db 662 -----AGAACTGCTGTTTGCTTACTGAGGCGCAAGGAGCAACGGTCAACCGTCTCTC 713

RESULT 8

US-10-682-845-68
; Sequence 68, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: LanzaVecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAMCD3 with M9 mutant in anti-CD3 part
US-10-682-845-68

Query Match 67.2%; Score 480; DB 18; Length 1479;
Best Local Similarity 81.5%; Pred. No. 2,1e-141;
Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

Qy 3 TATTGTATGATGACCCAGACTCCCAATTCTGCTGTATACAGCAGAGACAGGGTTACCAT 62
Db 3 TATCCAGGTGACCCAGTCTCAAAAATTCATGTCACATCAATAGAGAGACAGGGTCAGCGT 62
Qy 63 AACCTGCAAGGCCAGTCAAGTGTGATGATGATGTGGCTTGTGACCAACGAAAGCCAGG 122
Db 63 CACCTGCAAGGCCAGTCAAGTGTGATGATGATGTGGCTTGTGACCAACGAAAGCCAGG 122
Qy 123 GCAATCTCTTAAGACATGATTTACTCGGCATCTTACCGGTACAGTGGAGTCCCTGATCG 182
Db 123 GCAATCTCTTAAGACATGATTTACTCGGCATCTTACCGGTACAGTGGAGTCCCTGATCG 182
Qy 183 CTTCACTGCAAGTGGATATGAGAGCGAATTTCACTTTCACATCAGCACTGTGACAGCTGA 242
Db 183 CTTCACTGCAAGTGGATATGAGAGCGAATTTCACTTTCACATCAGCACTGTGACAGCTGA 242
Qy 243 AGACCTGGCACTTATTTCTGTCTGACAGAGATTATAGCT-----CGCTCGAAGGGG 293
Db 243 AGACCTGGCAAGATTATTTCTGTCTGACAGATTATAGCT-----CGCTCGAAGGGG 293
Qy 294 GACCAAGCTGGAATTAAGAGTGAAGCGGTTCACGCGGAGAGTGGCTTCGCGGTGCGG 353
Db 303 GACCAAGCTGGAATTAAGAGTGAAGCGGTTCACGCGGAGAGTGGCTTCGCGGTGCGG 353
Qy 354 ATGCAAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 413
Db 363 TTCTCAGGTGAATCTGACAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGT 422
Qy 414 CATCACTTGAAGTCTGCTGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 473
Db 423 CATCACTTGAAGTCTGCTGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 482
Qy 474 GCTTCGAGAAAGGCTCTGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 533
Db 483 GCTTCGAGAAAGGCTCTGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 542

QY 534 TAAATCGGCTTTATGTCCAGACTGAGCATCAGCAAGACAACCTCAAGAGCCAAAGTTT 593
| | | | |
Db 543 TAATGAGCTTTTATCCAGATCAGACATCAGAAAGACAATTCAGAGCCAAAGTTT 602
| | | | |
QY 594 CTTAAATAATGAACAGTCTGCAAACTGATGACACAGCATGTACTACTGTGCCAGTCCGAG 653
| | | | |
Db 603 CTTTAAATAATGAACAGTCTGCAAGCTATGACACAGCATGTATTAATCTGTCCAGAAATGG- 661
| | | | |
QY 654 GGGTAACCTAGGCGATCTTTGACTCTGGGGTCAAGGAACCTCAAGTCAACCGTCTCTC 713
| | | | |
Db 662 -----AGAACTGTGCTTGTCTTACTAGGGGCCAAGGACCAAGGTCAACCGTCTCTC 713
| | | | |

RESULT 9

US-10-682-845-70
; Sequence 70, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: LanzaVecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAMxCD3 with M10 mutant in anti-CD3 part
US-10-682-845-70

Query Match 67.2%; Score 480; DB 18; Length 1479;
Best Local Similarity 81.5%; Pred. No. 2,1e-141;

Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

QY 3 TATTTGATGATGACCCAGACTCCCAATTCCTGCTTGATGACAGAGACAGGGTTACCAT 62
| | | | |
Db 3 TATTCAGCTGACCCAGCTCAAAAATTCATGTCCACATCATGTAGAGACAGGGTCAAGCT 62
| | | | |
QY 63 AACCTGCAAGGCCAGTGAAGTGTGATGATGTGTGGCTTGGTACCAAGAAAGCCAGG 122
| | | | |
Db 63 CACCTGCAAGGCCAGTGAAGTGTGATGATGTGTGGCTTGGTACCAAGAAAGCCAGG 122
| | | | |
QY 123 GCAATCTCCGAAACCTGCTATATCTGTGATCCAAATCGCTACACTGAGTCCCTGATCG 182
| | | | |
Db 123 GCAATCTCCCTTAAGCACTGATTTTACTGCGATCTTACCGGTACAGTGGATCCCTGATCG 182
| | | | |
QY 183 CTTTCACTGCGAGTGAATATGGAAGATTTCACTTTCACATCAGCACTGTGACAGGCTGA 242
| | | | |
Db 183 CTTTCACTGCGAGTGAATATGGAAGATTTCACTTTCACATCAGCACTGTGACAGGCTGA 242
| | | | |
QY 243 AGACCTGGCAGTTTATTTCTGTCAAGCAGATTAATAGT-----CGCTCGAAGGGG 293
| | | | |
Db 243 AGACCTGGCAGATTAATTTCTGTCAAGCAATATTAACAGTATCCGCTCAAGTTCCGCTGG 302
| | | | |
QY 294 GACCAAGCTGGAATAAAGTGAAGCGGTTTCAGGCGAGGTGGCTCTGCGGGTGGCGG 353
| | | | |
Db 303 GACCAAGCTGGAATCAAAAGT 362
| | | | |
QY 354 ATGCAAGTGCAGGTGAAGAGTCAAGACCTGCGCTGTGGCGCTTCAACAGACCTGTCTC 413
| | | | |
Db 363 TTCTCAGGTGAATCAAGTCAAGAGTCAAGACCTGCGCTGTGCAAGACCTGTCTC 422
| | | | |
QY 414 CATCACTTGCACATCTCTCTGGGTTTTCATTAACCAATTAATGTGTGAATCTGTGGTCCCA 473
| | | | |
Db 423 CATCACTTGCACAGTCTCTGTGGTTCATTAACCAATTAATGTGTGAATCTGTGGTTCGCCA 482
| | | | |

QY 474 GCCTCCAGAAAGGCTCTGAGTGTGGGAGTAAATATGAGGCTGTGGAAGCAAAATTA 533
| | | | |
Db 483 GTTCCAGAAAGGCTCTGAGTGTGGGAGTAAATATGAGGCTGTGGAAGCAAAATTA 542
| | | | |
QY 534 TAAATCGGCTTTATGTCCAGACTGAGCATCAGCAAGACAACCTCAAGAGCCAAAGTTT 593
| | | | |
Db 543 TAATGAGCTTTTATCCAGATCAGACATCAGCAAGACAACCTCAAGAGCCAAAGTTT 602
| | | | |
QY 594 CTTAAATAATGAACAGTCTGCAAACTGATGACACAGCATGTACTACTGTGCCAGTCCGAG 653
| | | | |
Db 603 CTTTAAATAATGAACAGTCTGCAAGCTATGACACAGCATGTATTAATCTGTGCCAGAAATGG- 661
| | | | |
QY 654 GGGTAACCTAGGCGATCTTTGACTACTGAGGTCAAGGAACCTCAAGTCAACCGTCTCTC 713
| | | | |
Db 662 -----AGAACTGTGCTTGTCTTACTAGGGGCCAAGGACCAAGGTCAACCGTCTCTC 713
| | | | |

RESULT 10

US-10-682-845-72
; Sequence 72, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: LanzaVecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAMxCD3 with M11 mutant in anti-CD3 part
US-10-682-845-72

Query Match 67.2%; Score 480; DB 18; Length 1479;
Best Local Similarity 81.5%; Pred. No. 2,1e-141;

Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

QY 3 TATTTGATGATGACCCAGACTCCCAATTCCTGCTTGATGACAGAGACAGGGTTACCAT 62
| | | | |
Db 3 TATTCAGCTGACCCAGCTCAAAAATTCATGTCCACATCATGTAGAGACAGGGTCAAGCT 62
| | | | |
QY 63 AACCTGCAAGGCCAGTGAAGTGTGATGATGTGTGGCTTGGTACCAAGAAAGCCAGG 122
| | | | |
Db 63 CACCTGCAAGGCCAGTGAAGTGTGATGATGTGTGGCTTGGTACCAAGAAAGCCAGG 122
| | | | |
QY 123 GCAATCTCCGAAACCTGCTATATCTGTGATCCAAATCGCTACACTGAGTCCCTGATCG 182
| | | | |
Db 123 GCAATCTCCCTTAAGCACTGATTTTACTGCGATCTTACCGGTACAGTGGATCCCTGATCG 182
| | | | |
QY 183 CTTTCACTGCGAGTGAATATGGAAGATTTCACTTTCACATCAGCACTGTGACAGGCTGA 242
| | | | |
Db 183 CTTTCACTGCGAGTGAATATGGAAGATTTCACTTTCACATCAGCACTGTGACAGGCTGA 242
| | | | |
QY 243 AGACCTGGCAGTTTATTTCTGTCAAGCAGATTAATAGT-----CGCTCGAAGGGG 293
| | | | |
Db 243 AGACCTGGCAGATTAATTTCTGTCAAGCAATATTAACAGTATCCGCTCAAGTTCCGCTGG 302
| | | | |
QY 294 GACCAAGCTGGAATAAAGTGAAGCGGTTTCAGGCGAGGTGGCTCTGCGGGTGGCGG 353
| | | | |
Db 303 GACCAAGCTGGAATCAAAAGT 362
| | | | |
QY 354 ATGCAAGTGCAGGTGAAGAGTCAAGACCTGCGCTGTGGCGCTTCAACAGACCTGTCTC 413
| | | | |
Db 363 TTCTCAGGTGAATCAAGTCAAGAGTCAAGACCTGCGCTTAATGTGCAAGACCTGTCTC 422
| | | | |

Qy 414 CATCACTTGCAGCTGTCTTGCGTTTTCATTAAACCAATTATGCTGTACCTGGGTTCCGCA 473
Db 423 CATACCTGCAGACACTCTCTGGTTTCTCACTTAAGCTATGGTGTACCTGGGTTCCGCA 482
Qy 474 GCCTCCAGAAAGGGTCTGAGTGGCTGGAGTATATGAGGCTGGTGGAGCACAAAATTA 533
Db 483 GTCTCCAGAAAGGGTCTGAGTGGCTGGAGTATATGAGGCTGGTGGAGCACAAAATTA 542
Qy 534 TAAATCGGCTTTATGTCAGACTGAGCATCAGACAGCAACTCCAGAGCCAAATTTT 593
Db 543 TAAATCGGCTTTATGTCAGACTGAGCATCAGACAGCAACTCCAGAGCCAAATTTT 602
Qy 594 CTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGATCTACTGTCCAGTCCGGG 653
Db 603 CTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGATCTACTGTCCAGATGG- 661
Qy 654 GGGTAAGTACGCGCTATGCTTGGACTACTGAGGCTCAAGAGAACTCAGTCAAGTCTCTC 713
Db 662 -----AGAACTGGTGTGTTGCTTACTGGGGCCAGAGGACCAAGGTCACCGTCTCTC 713

RESULT 11
US-10-682-845-74
; Sequence 74, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzevecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAmxCD3 with M13 mutant in anti-CD3 part
US-10-682-845-74

Query Match 67.2%; Score 480; DB 18; Length 1479;
Best Local Similarity 81.5%; Pred. No. 2,1e-141;
Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

Qy 3 TATTGTATGATACCAAGCTCCCAATTCCTGCTGTATCAGACAGAGACAGGGTTACCAT 62
Db 3 TATCACCTGCAGCCAGTCTCAAAAATTCATGTCCACATCAGTAGAGACAGGGTCAAGGT 62
Qy 63 AACCTGGAAGGCCAGTCAAGTGTGAGTAATGATGAGTGGCTTGTATCCAAAGAGAGCCAG 122
Db 63 CACCTGGAAGGCCAGTCAAGTGTGAGTAATGATGAGTGGCTTGTATCCAAAGAGAGCCAG 122
Qy 123 GCAATCTCCGAAATGCTGATATATCTGTCATCCAAATGCTCACTGGAGTCCCTGATCG 182
Db 123 GCAATCTCCGAAATGCTGATATATCTGTCATCCAAATGCTCACTGGAGTCCCTGATCG 182
Qy 183 CTTCACTGGCAGTGGATATGAGGAGCGAATTCATCTTCCATCAGACTGTGACAGGCTGA 242
Db 183 CTTCACTGGCAGTGGATATGAGGAGCGAATTCATCTTCCATCAGACTGTGACAGGCTGA 242
Qy 243 AGACTGGCAGTGGATATGAGGAGCGAATTCATCTTCCATCAGACTGTGACAGGCTGA 293
Db 243 AGACTGGCAGTGGATATGAGGAGCGAATTCATCTTCCATCAGACTGTGACAGGCTGA 293
Qy 294 GACCAAGCTGGAATTAAGAGTGGAGCGGCTTCAGGCGAGAGTGGCTTCGCGGCTGGCGG 353
Db 294 GACCAAGCTGGAATTAAGAGTGGAGCGGCTTCAGGCGAGAGTGGCTTCGCGGCTGGCGG 353
Qy 303 GACCAAGCTGGAATTAAGAGTGGAGCGGCTTCGCGGCGAGAGTGGCTTCGCGGCTGGCGG 362
Db 303 GACCAAGCTGGAATTAAGAGTGGAGCGGCTTCGCGGCGAGAGTGGCTTCGCGGCTGGCGG 362

Qy 354 ATGCAAGTGCAGGTGAAGAGTCAAGACCTGGCTGTGGTCCGCTTCCAGAGCTGTCTC 413
Db 363 TTCTCAGAGTGAAGAGTCAAGAGTCAAGACCTGGCTGTGGTCCGCTTCCAGAGCTGTCTC 422
Qy 414 CATCACTTGCAGCTGTCTGGGTTTTCATTAAACCAATTATGAGTGTACAGTGGTTCGCCA 473
Db 423 CATCACTTGCAGCTGTCTGGGTTTTCATTAAACCAATTATGAGTGTACAGTGGTTCGCCA 482
Qy 474 GCCTCCAGAAAGGGTCTGAGTGGCTGGAGTATATGAGGCTGGTGGAGCACAAAATTA 533
Db 483 GTCTCCAGAAAGGGTCTGAGTGGCTGGAGTATATGAGGCTGGTGGAGCACAAAATTA 542
Qy 534 TAAATCGGCTTTATGTCAGACTGAGCATCAGACAGCAACTCCAGAGCCAAATTTT 593
Db 543 TAAATCGGCTTTATGTCAGACTGAGCATCAGACAGCAACTCCAGAGCCAAATTTT 602
Qy 594 CTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGATCTACTGTCCAGTCCGGG 653
Db 603 CTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGATCTACTGTCCAGATGG- 661
Qy 654 GGGTAAGTACGCGCTATGCTTGGACTACTGAGGCTCAAGAGAACTCAGTCAAGTCTCTC 713
Db 662 -----AGAACTGGTGTGTTGCTTACTGGGGCCAGAGGACCAAGGTCACCGTCTCTC 713

RESULT 12
US-10-682-845-76
; Sequence 76, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzevecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAmxCD3 with M14 mutant in anti-CD3 part
US-10-682-845-76

Query Match 67.2%; Score 480; DB 18; Length 1479;
Best Local Similarity 81.5%; Pred. No. 2,1e-141;
Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

Qy 3 TATTGTATGATACCAAGCTCCCAATTCCTGCTGTATCAGACAGAGACAGGGTTACCAT 62
Db 3 TATCACCTGCAGCCAGTCTCAAAAATTCATGTCCACATCAGTAGAGAGAGGGTCAAGGT 62
Qy 63 AACCTGGAAGGCCAGTCAAGTGTGAGTAATGATGAGTGGCTTGTATCCAAAGAGAGCCAG 122
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Qy 123 GCAATCTCCGAAATGCTGATATATCTGTCATCCAAATGCTCACTGGAGTCCCTGATCG 182
Db 123 GCAATCTCCGAAATGCTGATATATCTGTCATCCAAATGCTCACTGGAGTCCCTGATCG 182
Qy 183 CTTCACTGGCAGTGGATATGAGGAGCGAATTCATCTTCCATCAGACTGTGACAGGCTGA 242
Db 183 CTTCACTGGCAGTGGATATGAGGAGCGAATTCATCTTCCATCAGACTGTGACAGGCTGA 242
Qy 243 AGACTGGCAGTGGATATGAGGAGCGAATTCATCTTCCATCAGACTGTGACAGGCTGA 293
Db 243 AGACTGGCAGTGGATATGAGGAGCGAATTCATCTTCCATCAGACTGTGACAGGCTGA 293
Qy 294 GACCAAGCTGGAATTAAGAGTGGAGCGGCTTCAGGCGAGAGTGGCTTCGCGGCTGGCGG 353
Db 294 GACCAAGCTGGAATTAAGAGTGGAGCGGCTTCAGGCGAGAGTGGCTTCGCGGCTGGCGG 353
Qy 303 GACCAAGCTGGAATTAAGAGTGGAGCGGCTTCGCGGCGAGAGTGGCTTCGCGGCTGGCGG 362
Db 303 GACCAAGCTGGAATTAAGAGTGGAGCGGCTTCGCGGCGAGAGTGGCTTCGCGGCTGGCGG 362

OY 224 GACCAAGCTGGAATTAAGGTGAGGCGGTTACGCCGAGAGTGGGCTCTGCGCGTGGCCG 353
 Db 303 GACCAAGCTCGAGATCAAAAGGTGGTGTGGTTCCTGACCGGGCGGCTCCCGTGGTGG 362
 OY 354 ATCGAGGTGCAGGTGAGAGAGTCAAGACCTGGCTGTGGCCGCTCAAGAGCCGTGC 413
 Db 353 TTCTCAGGTGAACCTGCAGAGGTCAAGAGCCTGGCTTAGTGCAGCCTCTCAAGAGCCGTGC 422
 OY 414 CATCACTTGCACTGTCTCGGGTTTCAATTACCAATTATGTGTACCTGGGTTGGCA 473
 Db 423 CATCACTTGCAAGTCTCTGGTTTCTCATTAATCACTTAGTGTACACTGGGTTGGCA 482
 OY 474 GCGTCAAGGAAGGGCTGGAAGGTGGGAGTAATGTGGCTGTGGAGGACAATTA 533
 Db 483 GTCTCAAGGAAGGGCTGGAAGGTGGGAGTAATGTGGAGTGTGGAGGACAAGCTTA 542
 OY 534 TAATTGGCTTTATGTCCAGACTGAGCATTCAGCAAGACAACCTCCAAAGGCCAAGTTT 593
 Db 543 TAATCAGCTTTCATATCCAGACTGAGCATTCAGCAAGACAATTCAAAGGCCAAGTTT 602
 OY 594 CTTAAAAATGAACAGCTGTCGAAACTGATGACACGCCATGTACTACTGTGCCAGTGGGG 653
 Db 603 CTTAAAAATGAACAGCTGTCGAAACTGATGACACGCCATATATTACTGTGCCAAGATGG- 661
 OY 654 GGGTAACTAAGCGCTATGCTTTGGACTACGTGGGTCAAGGAACCTCAGTCAACCGTCTCTC 713
 Db 662 -----AGAACTGGTCTGTTCTTACGTGGGGCCAAAGGACCAAGGTCACCGTCTCTC 713

RESULT 13
US-10-682-845-78

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sequence /8, Application US/10682845
Publication No. US2004016241A1
GENERAL INFORMATION:
APPLICANT: Lanzavecchia, Antonio
TITLE OF INVENTION: Potent T cell modulating molecules
FILE REFERENCE: G2296 US
CURRENT APPLICATION NUMBER: US/10/682,845
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.1
SEQ ID NO 78
LENGTH: 1479
TYPE: DNA
ORGANISM: artificial sequence
FEATURES:
OTHER INFORMATION: scFv EPCAMxCD3 with M20 mutant in anti-CD3 part
US-10-682-845-78

```

Query Match	67.2%	Score 480	DB 18	Length 1479
Best Local Similarity	81.5%	Pred. No. 2.1e-141		
Matches 587; Conservative	0	Mismatches 115	Indels 18	Gaps 2

QY	3	TATTTGTATGATCCAGACTCCCAATTCCTGCTTGTATCAGCAGGAGACAGGGTTACCAT	62
Db	3	TATCCAGCTGACCCCAAGTCTCAAAAATTCAATGTCACATCAGTAGGAGACAGGGTCAAGCGT	62
QY	63	AACCTGCAAGGCGCACTGACAGTGTGAGTATGATGTGGCTTGATCAACACAGAAAGCAGG	122
Db	63	CACCTGCAGAGCGCACTGAGAAATGTGGGTACTAATGTAGGCTGGTATCAACAGAAACAGG	122
QY	123	GCAGTCTCCGAAACTGCTGATATTACTCTGTGCATCCAAATGCGTCACTAGAGTCCCTGATCG	182
Db	123	GCAATCTCTTAAAGCACTGATTTTAACTCGGCATCTCAACGGTACAGTGGAGTCCCTGATCG	182
QY	183	CTTCACTGCGAGTGGATATATGGGACCGATTTCACTTTACCATCAGACACTGTGTGAGGCTGA	242
Db	183	CTTCCACAGGCAATGATCTGTGGGACAGATTTCACTCTCAACATCAGCAATATGTGAGTCTGA	242

QY	243	AGACCTGGGATGTTATTTCTGTCCAGCAGGATTAATAGCT-----CGCTCGGAGGGG	239
Db	243	AACTCTGGGAGGATATTTCTGTCCAGCAATATTAACACTATCCGCTCAGCTTCGGTGTGG	3020
QY	294	GACCAAGCTGAGAAATPAAAGTGGAGCGGTTCCAGCGGAGGTGGCTCTGGCGGTGGCGG	3538
Db	303	GACCAAGCTCGAGATCCAAAGTGGTGGTTCCTGGCGCGGGCGGCTCCGGTGGTGGTG	3632
QY	354	ATGCAAGTGCAGGTGGAGGAAGTCAAGAACCTGGGCTGTGGCGGCTCACAGAGCTGTCT	4138
Db	363	TTCCTAGGTGAACCTGCAGAGATCAAGAACCTGGGCTGTGGCGGCTCACAGAGCTGTCT	4222
QY	414	CATCACTTGCACTGTCTCTGGGTTTTCAATTAACAATTAATGGGTACACTCGGGTTGGCCA	4737
Db	423	CATCACTTGCAAGTCTCTGGGTTTTCAATTAACACTGTATGGGTGTACACTGGGTTGGCCA	4823
QY	474	GCCTCCAGGAAGGGTCTTGAGTGGCTGGAGATTAATATGGGCTGTGGAGACCAAAATTA	5338
Db	483	GTCTCCAGGAAGGGGCTTGAGTGGCTGGAGATTAATGGAGGTGTGGAGACCAAGCTTA	5424
QY	534	TAAATTCGGCTCTATGTCCAGACTAGAGCTATCGACCAAGGACCAATCCAAAGGCCAAGTTT	5938
Db	543	TAAATTCGGCTCTATGTCCAGACTAGAGCTATCGACCAAGGACCAAAATCCAAAGGCCAAGTTT	6022
QY	594	CTTAAAAATGAAACAGTCTGCCAACTGATGACACAGCCATGTACTACTGTGCCAGTGGGG	6538
Db	603	CTTAAAAATGAAACAGTCTGCCAACTGATGACACAGCCATATATTAATCTGTGCCAAGATGG-	6618
QY	654	GGGTAACTAAGGCTATGCTTTGGACTACTGTGGGTCAAAGAACTCAGTCAAGCTCTCTCTC	7138
Db	662	-----AGAACTGTGTGTTTCTTACTCTGGGGCCAAAGGAACTCAGTCAAGCTCTCTCTC	7138

Db

662 -----AGACTGTCGTCGTTTGCTTACTGGGGCCAGAGGACCAACGGTCACCGTCTCTC 713

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RESULT 14
US-10-682-845-80
; Sequence 80, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAMxCD3 with M1 mutant in anti-CD3 part
US-10-682-845-80

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Query Match 67.2%; Score 480; DB 18; Length 1479;

	Matches	58%;	Conservative	0;	Mismatches	115;	Indels	18;	Gaps	2
QY	3	TATTGTATGACCCAGACTCCCAAATTCCTCTGTATACACAGAGAGA CAGGGTACAT	62							
Db	3	TATCCAGGTGACCCAGGTCTCAAAAATTTCATGTCACATCAGTAGGAGACAGGGTCAGCGT	62							
QY	63	AACTGCGAAGGCCAGTCAAGTGTGAGTAAAGATGTGGCTTGTCACAAACGAACCCAG	122							
Db	63	CACCTGCAAGGCCAGTCAAGATGTGGGTCTAAATGTAACCTGTGTACACMAAACCGG	122							
QY	123	GCAGTCTCCGAAACTGCTGATATATCTGTGATCCAGTGCCTACACTGAGAGTCCCTGATCG	182							
Db	123	GCATATCTCTAAAGACATGATTATCTCGGCACTCCACCGGTACAGTGGAGTCCCTGATCG	182							

Oy	183	CTTCACTGGCACTGGATATAGGGACCGAATTTCACTTTACATCATAGACACTGGACGCTGA	242
Db	183	CTTCACTGGCACTGGATATAGGGACCGAATTTCACTTTACATCATAGACACTGGACGCTGA	242
Oy	243	AGACCTGGCAGTTTATTTCTGTCTGTCAGCAGGATTAATAGCT-----CGCTCGGAGGAGG	293
Db	243	AGACTTGGCAGAGTATTTCTGTCTGTCAGCAATATTAACACTATTCGCGTCACGTTGGGTCTGG	302
Oy	294	GACCAAGCTGGAAATATAAAGGTGGAGGCGGCTTCAGCGGAGAGTGGTCTTGGCGGTGGCGG	353
Db	303	GACCAAGCTCGAGATCAAAAGGTGGTGGTGTCTTGGCGGCGGCGGCTTCGCGGTGGGTGG	362
Oy	354	ATTCGAGGTCGAGGTGGAAGAGAGTCAAGACCTGGCGCTGGTGGCGGCTTCACAGAGCTGTCTC	413
Db	353	TTCTCAAGTGGAAATCTGCAGAGATCAAGACCTGGCGCTAGTGCAGCCCTTCACAGAGCTGTCTC	422
Oy	414	CATCACTTGCACCTGTCTCTCGGCTTTTCATTAAACCAATTATGTGTACACTGGGTTGCCA	473
Db	423	CATCACTTGCACAGTCTCTGTTTCTCATTTAATACCTATATGGTACACTCGGGTTGCACA	482
Oy	474	GCCTTCAGGAAGAGGCTTGGAGATGGCTGGGAGTAAATATGGGCTGTGGAAAGCAACAATTA	533
Db	483	GTCTTCAGGAAGAGGCTTGGAGATGGCTGGGAGTAAATATGGAGTGGAGTGAAGCAACAACTA	542
Oy	534	TAAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGACAACACTCCAGAGCCAAAGTTT	593
Db	543	TATATCAGCTTTCAATATCCAGACTGAGCATCAGCAAGACAATTCAGAGCCAAAGTTT	602
Oy	594	CTTAAAAATGAACAGTCTTGCAAACTGATGATGACACAGCCATGTACTGTGTCAGTCCGAGG	653
Db	603	CTTTAAAAATGAACAGTCTTGCAAACTGATGATGACACAGCCATATATTACTGTGCCAGATGG-	661
Oy	654	GdGTAACTAAGCGCTATGCTTTTGAGACTACATGCGGGTCAAGAAACCTCACTACCGCTCTCC	713
Db	662	-----AGAACTGGTCTGTTTGTCTTACTGCGGGCCAAAGGAAACCAAGCATCGCTCTCTC	713
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US-10-682-845-82			
Sequence 82, Application US/10682845			
Publication No. US20040162411A1			
GENERAL INFORMATION:			
APPLICANT: Lanzavecchia, Antonio			
TITLE OF INVENTION: Potent T cell modulating molecules			
FILE REFERENCE: G2296 US			
CURRENT APPLICATION NUMBER: US/10/682,845			
CURRENT FILING DATE: 2003-10-10			
PRIOR APPLICATION NUMBER: US 60/419,149			
PRIOR FILING DATE: 2002-10-18			
PRIOR APPLICATION NUMBER: CA 2,403,313			
PRIOR FILING DATE: 2002-10-11			
NUMBER OF SEQ ID NOS: 89			
SOFTWARE: PatentIn version 3.1			
SEQ ID NO 82			
LENGTH: 1479			
TYPE: DNA			
ORGANISM: artificial sequence			
FEATURE:			
OTHER INFORMATION: scFv EpcAMxCD3 with M58 mutant in anti-CD3 part			
US-10-682-845-82			

	Score	DB	Length
Query Match	67.2%	480	1479
Best Local Similarity	81.5%		
Matches 587; Conservative		2.1e-141	
		0; Mismatches 115;	Indels 18; Gaps 2

Qy 3 TATTGATGAGCCAGACATCCCAATTCCTGGCTGTATCAGCAGGAGACAGGGTTACAT 62

Db 3 TATCAGATGACCCCACTCTCAAAAATTCAATGTCACATCAGTGAAGACAGGGTCAAGCT 62

Qy 63 AACCTGCAGGCGCAGTCAGAGTGTGATGATGATGATGCTGGCTGTACCAACAGAGCGAG 122

Db 63 CACCTGCAGGCGCAGTCAGAAATGTGGTACTAATGTAGCCTGGTATTAACAAGAAACAG 122

QY	123	GCAGTCTCCGAAACGTGCTGATATATACCTCTGCATTCACATCGCTCACTGAGATCCCTATCG	182
Db	123	GCAATCTCTTAAGACATGATTTACTCTGGCATCTCAACGGTACAGTGAATCCCTGATCG	182
QY	183	CTTCACTGGCAGTGGATATATGGACCGAATTTCACTTTACATTCAGCATCTGTGAGGCTGA	242
Db	183	CTTCAACAGGACAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATGTGCAGTCTGA	242
QY	243	AGACTCTGGCAGTTTATTTCTGTCTGACAGGATTAATAGCT-----CGCTCGGAGGGG	293
Db	243	AGACTCTGGCAGGATATTTCTGTCAACAATATAACAGCTATCCGCTCAGCTTCCGATCTGG	302
QY	294	GACCAAGCTGCAAAATATAAAGGTGAGGCGGCTTCAGCGGAGGGGTCTTGGCCGCTGACG	353
Db	303	GACCAAGCTCGAGATCAAAAGGTGTGTGTCTTGGCCGCGGCGGCTTCCGATGTGTGG	362
QY	354	ATCGCAGGTGCAGGTGAAAGGAGTCAAGACCTGGCCCTGTGTGGCGCTCTCAACAGACCTGTC	413
Db	353	TTCTCAGGTGAAACGTGCAGGAGTCAAGACCTGGCTGATGTGCAAGCCTCAACAGACCTGTC	422
QY	414	CATCACTTGCACGTGTCTGTGGGTTTTCAATTAACCAATTAATGTGTGACACTGGGTTGGCCA	473
Db	423	CATCACTGCACAGTCTGTGGTTTTCTAATTAATGACTATGTGTGTACACTGGGTTGGCCA	482
QY	474	GCCTCCAGAAAGGGTCTGGAATGTGCTGGGAAATATATGCGCTGTGTGAAAGCAAAATTA	533
Db	483	GTCTCCAGAAAGGGTCTGGAATGTGCTGGGAAATGATGAGAGTGTGAAAGCACAGACTTA	542
QY	534	TAAATTCGGCTCTTATGTCCAGACTAGCAATCAAGCAAGACAACTCCAAAGGCCAAATTTT	593
Db	543	TAAATTCGGCTCTTATGTCCAGACTAGCAATCAAGCAAGACAAATTTCCAAAGGCCAAATTTT	602
QY	594	CTTAAAAATGAACAGTCTTGCAAACTGATGACACAGCCATGTACTACTGTGCCAGTCGGGG	653
Db	603	CTTAAAAATGAACAGTCTTGCAAGCTAATGACACAGCCATATATTACTGTGCCAGAAATGG-	661
QY	654	GGGTAACTACGGCTATGCTTTTGGACTACGTGGGGTCAAGAACTCTAGTACCGGCTTCCTC	713
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Search completed: February 19, 2005, 02:16:20
Job time : 466.528 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 20:04:30 : Search time 2561.12 Seconds
(without alignments) 10611.722 Million cell updates/sec

Title: US-10-075-947A-2

Perfect score: 714

Sequence: 1 agtatgttgatgaccagac.....cctcagtcaccgtctctca 714

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_est4:
5: gb_est5:
6: gb_est6:
7: gb_est7:
8: gb_est8:
9: gb_est9:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	280.8	39.3	594	2	BE309592 601094848
6	276	38.7	691	2	BF578188 602094691
7	265.4	37.2	970	5	BQ940476 AGENCOURT
8	262.4	36.8	831	9	CR047446 Forward B
9	262.4	36.8	930	2	BF579344 602095631
10	259	36.3	792	7	CO567792 AGENCOURT
11	257.4	36.1	793	7	CO574382 AGENCOURT
12	253	35.4	914	7	CO558560 AGENCOURT
13	250.4	35.1	883	2	BF580610 602093730
14	250	35.0	912	5	BUS22894 AGENCOURT
15	247	34.6	664	6	BF733751 BY733751
16	245.4	34.4	831	7	CO562833 AGENCOURT
17	244.6	34.3	767	7	CO562905 AGENCOURT
18	243.6	34.1	520	2	AW917371 EST348675
19	243.4	34.1	742	7	CO567469 AGENCOURT
20	242.8	34.0	685	8	BH275985 AGENCOURT
21	242.4	33.9	899	4	BG973020 602838676
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ALIGNMENTS

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DEFINITION 603309721.F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5345741 5', mRNA sequence.
ACCESSION B1690298
VERSION B1690298.1 GI:15652927
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 840)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LLM11878 row: 1 column: 06
High quality sequence stop: 828.

FEATURES

SOURCE

1. 840

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/mol_type="mRNA"

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/db_xref="taxon:10090"

/clone="IMAGE:5345741"

/sex="female, virgin"

/tissue_type="infiltrating ductal carcinoma"

/dev_stage="5 months"

/lab_host="DH10B"

/clone_lib="NCI CGAP Mam6"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI. Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies, Inc. Investigator providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Query Match 43.7%; Score 312; DB 4; Length 840;
Best Local Similarity 89.4%; Pred. No. 7.4e-80;

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QY	339	CTCTGGCGGTGGCGGATGCGACAGTGCAGGTGAAGAGTGCAGACCTGGCTGTGGCGCC								398
Db	57	CCCAAGCGTATCCCTTTCCACAGGTGCAGCTGACAGACAGTCCAGGCTGAGTGGCGCC								116
QY	399	CTCACAAGCGCTGTCCATCATCTTGACATGTCTCTGGGGTTTTCATTAAACCAATTATGGGT								458
Db	117	CTCACAAGCGCTGTCCATCATCATGCACTGTCTCTGGGTTCTCATTTAACCAACTATGGGT								176
QY	459	ACACTGGGTTGGCGCAGCCTCCAGAAAAGGTCGTGAGTGGCTGGAGATTAATATGGCTGG								518
Db	177	AGACTGGGTTGGCGCAGCTCCAGGAAAAGGCTGGAAGTGGCTGGAGATGATATGGGGTGG								236
QY	519	TGGAAGCAAAATTATTAATTTCGGCTCTTATGTCCAGACTAGCATCAGCAAGAACAACTC								578
Db	237	TGGAAGCAAAATTATTAATTTCAGGCTCTCAATTCCAGATGAGCATCAGCAAGAACAACTC								296
QY	579	CAAGAGCCAAATTCTTAAAAATGACACGCTGCAATCTGATATGACACAGCCATGTACTA								638
Db	297	CAAGAGCCAAATTCTTAAAAATGACACGCTGTCAACTATATGACACAGCCATGTACTA								356
QY	639	CTGTGCGCAGTGGGGGGGTAACTACGCGCTATGCTTTGGACTACTTGGGTCAAGAACTC								698
Db	357	CTGTGCGCAGTGGGGGGGTACTTAACGAGAGGTGTATGACTAACTGGGGTCAAGAACTC								416
QY	699	AGTCACCGCTCTCTCA	714							
Db	417	AGTCACCGCTCTCTCA	432							

RESULT 2	BUS22581	LOCUS	BUS22581	861 bp	mRNA	linear	EST 13-SEP-2002
DEFINITION	AGNCOURT_10154040 NCI CGAP Co24 Mus musculus CDNA clone						
ACCESSION	BUS22581						
VERSION	BUS22581.1 GI:22830107						
KEYWORDS	EST.						
SOURCE	Mus musculus (house mouse)						
ORGANISM	Mus musculus						

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 861)	NIH-MGC http://mgc.ncbi.nlm.nih.gov/ .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.			

Tissue Procurement: The Cepho Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MSC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: L1AM14128 row: j column: 18
 High quality sequence stop: 723.

FEATURES	Location/Qualifiers
source	1. .861

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/lab_host="DH10B (r1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: oligo dT
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."

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Query Match	39.9%	Score 285	DB 5	Length 861
Best Local Similarity	87.1%	Pred. No. 6.1e-72		
Matches 325	Conservative 1	0	Mismatches 45	Indels 3
				Gaps 1
QY	345	CGGTGCGGATGCGAGGTGCGAGTGAAGGAGTCAAGACTGGCTGTGTCGCGCCTTACA	404	
Db	61	CTGTGTCTCTGTCCAGGTGCGAGTGTGCAAGGACAGGACTGGCTGTGTCGCGCCTTACA	120	
QY	405	GAGCTGTGCATCACTTGCACTGTCTCTGGGTTTTCATTACCAATTATGTGTACTGTG	464	
Db	121	GAGCTGTGCATCACTATGCAATGCAATGCTGTGCAAGGTTTCATTAAACGATATGATATCACTG	180	
QY	465	GGTTGCGCAGCCTCCAGGAAAGGCTCTGAGATGTGCTGGAGTAAATATGAGCTGTGGAAG	524	
Db	181	GGTTGCGCAGCCTCCAGGAAAGGCTCTGAGATGTGCTGTGATATGATGAGATGAGGAAG	240	
QY	525	CACAAATTATATTTGCGCTCTTATGTCCAGACTGATGATCGCAAGGACCACTCCAAAG	584	
Db	241	CACAAACTATATTTGCGCTCTTCAATCCAGACTGATGATCGCAAGGACCACTCCAAAG	300	
QY	585	CCAAGTTTCTTAAAAATGAACAGTCTGCGCAACTGATGACACAGCCATGTACTACTGTC	644	
Db	301	CCAAGTTTCTTAAACATTGAACAGTCTTCCAAACTGATGACACAGCCATGTACTACTGTC	360	
QY	645	GAGTC--GGGGGGGATTACTACGGCTATGCTTTGGACTACTGGGGTCAAGGAACCTCAGT	701	
Db	361	CAGACTGTGTACTATGATGGTGCCTCATATGCTATGGACTACTGGGGTCAAGGAACCTCAGT	420	
QY	702	CACCGTCTCTCTCA 714		
Db	421	CACCGTCTCTCTCA 433		

RESULT 3	480 bp	EST 19-NOV-2005
CAS77562		
LOCUS		
DEFINITION		
K0711809-5N NIA Mouse Hematopoietic Stem Cell (L1m1/-c-Klt-/Sca-1-)		
cDNA Library (Long) Mus musculus cDNA clone NIA:K0711809		
IMAGE:30074612 5', mRNA sequence.		

ACCESSION	CA577562
VERSION	CA577562.1
KEYWORDS	GI:25125953
SOURCE	BST.
ORGANISM	Mus musculus (house mouse)
	Mus musculus

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 480)	Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Alba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.	Systematic Analyses of NIA Mouse Hemopoietic Stem Cell (lin-/c-kit-/Sca-1-) cDNA library (Longo)

COMMENT
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6620, USA
Email: cdna@igsun.gic.nia.nih.gov
Plate: K0711 row: B column: 09
Seq primer: M13 Reverse
High quality sequence stop: 480
POLYA=No.

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FEATURES
  source
    location/Qualifiers
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      /organism="Mus musculus"
      /mol_type="mRNA"
      /strain="C57BL/6NCr"
      /db_xref="nigast:K0711B09-5N"
      /db_xref="taxon:10090"
      /clone="NIA:K0711B09 IMAGE:30074612"
      /tissue_type="Hematopoietic Stem Cell
      (lin-/C-Kit-/Sca-1-)"
      /dev_stage="Age approx.10 weeks old"
      /lab_host="DH10B"

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/clone.lib="NIA Mouse Hematopoietic Stem Cell
(lin-/C-Kit-/Sca-1-) cDNA library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (<http://19sun-grc.nia.nih.gov/cDNA>). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
obtained from Drs. Dennis Teub, Dan Longo (National
Institute on Aging, USA), Jonathan Keller (National Cancer
Institute, USA). Double-stranded cDNAs were synthesized
with an Oligo(dT) primer (Invitrogen):
5'-TGACTGAGTCTGAGTCCGAGCGCCCTTTTCTTTTCTTTT-3' from
0.9 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer SalI-S. The
products were purified by phenol/chloroform and ligated
into the cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.1 kb. The library was constructed
by Yulan Piao (NIA)."

ORIGIN

Query Match 39.8%; Score 284; DB 6; Length 480;
Best Local Similarity 86.2%; Pred. No. 1e-71;
Matches 326; Conservative 0; Mismatches 50; Indels 2; Gaps 1;

QY 339 CTCTGGCGGTGGCGGATGCGAGTGAAGAGTCCAGTCCGCTGGTGGCC 398
DB 7 CCCAAGCTGTGTCTTACCCAGTGCAGTGAAGAGTCCAGTCCGCTGGTGGCC 66
QY 399 CTCACAGAGCTGTTCATCATCTGACGTCTGGTTCATTACCAATTATGGGT 458
DB 67 CTCACAGAGCTGTTCATCATCTGACGTCTGGTTCATTACCAATTATGGGT 126
QY 459 ACAGTGGGTGGCGGAGCTCCAGAAAGGCTGAGTGGCTGAGTAATATGGCTGG 518
DB 127 ACAGTGGGTGGCGGAGCTCCAGAAAGGCTGAGTGGCTGAGTAATATGGCTGG 186
QY 519 TGGAAAGCAAAATTAATTTGGCTTTATGTCAGACTAGCATCAGCAAGACATC 578
DB 187 TGGAAAGCAAAATTAATTTGGCTTTATGTCAGACTAGCATCAGCAAGACATC 246
QY 579 CAAGAGCCAAAGTTTCTTAAATAATGAAGTCTGAAATCTAGTACAGAGCATGTA 638
DB 247 CAAGAGCCAAAGTTTCTTAAATAATGAAGTCTGAAATCTAGTACAGAGCATGTA 306
QY 639 CTGTGCGAGTGGGGG--GGTAACTACCGCTATGCTTTGACTATGGGGTCAAGAAC 696
DB 307 CTGTGCGAGTGGGGGTTACTACGTGAAGAGATGCTATGAGACTATGGGGTCAAGAAC 366
QY 697 TCAGTCAACCGTCTCTCA 714
DB 367 TCAGTCAACCGTCTCTCA 384

RESULT 4

LOCUS BF182141 671 bp mRNA linear EST 31-OCT-2000
DEFINITION 601804682P1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4035429 5',
mRNA sequence.

ACCESSION BF182141
VERSION BF182141.1 GI:11060283
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 671)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-romail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc. (LNLN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: L1AM9309 row: d column: 22
High quality sequence stop: 669.

FEATURES

SOURCE

1. 671
Location/Qualifiers

/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:4035429"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone.lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

ORIGIN

Query Match 39.7%; Score 283.4; DB 2; Length 671;
Best Local Similarity 84.0%; Pred. No. 1.7e-71;
Matches 320; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 334 GGTGGCTTGGCGGTGGCGGATGCGAGTGAAGAGTCCAGTCCGCTGGTGG 393
DB 34 GCTTTCACAAAGTTTACCTGTGCTCCAGTGAAGAGTCCAGTCCGCTGGTGG 93
QY 394 GCGGCTTCACAGAGCTGTTCATCATCTGACGTCTGGTTCATTACCAATAT 453
DB 94 GCGGCTTCACAGAGCTGTTCATCATCTGACGTCTGGTTCATTACCAATAT 153
QY 454 GGTGTACACTGGTGGCGGAGCTCCAGAAAGGCTGAGTGGCTGGAATATGG 513
DB 154 GATATACTGATTCGCAAAACACAGAAAGGCTGAGTGGCTGGAATATATGG 213
QY 514 GCTGTGGAACAAATTAATTTGGCTTTATGTCAGACTAGCATCAGCAAGAC 573
DB 214 ATGGGTGAGACAAATTAATTTGGCTTTATGTCAGACTAGCATCAGCAAGAC 273
QY 574 AACTCCAAGAGCAAGTTTCTTAAATAATGAAGTCTGAAATCTAGTACAGAGCAT 633
DB 274 AACTCCAAGAGCAAGTTTCTTAAATAATGAAGTCTGAAATCTAGTACAGAGCAT 333
QY 634 TACTACTGTGCGAGTGGGGGTTACTACGTGAAGAGATGCTATGAGACTATGGGGTCAAGAAC 693
DB 334 TACTACTGTGGAACGCTCAGTGTGATGCTTATGAGACTATGGGGTCAAGAAC 393
QY 694 AACTCAAGTCAACCGTCTCTCA 714
DB 394 AACTCAAGTCAACCGTCTCTCA 414

RESULT 5

LOCUS BE309592 594 bp mRNA linear EST 26-OCT-2000
DEFINITION 601094848P1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3489635 5',
mRNA sequence.

ACCESSION BE309592
VERSION BE309592.1 GI:9168025

KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 594)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LLM6530 row: 0 column: 12
High quality sequence stop: 591.
Location/Qualifiers

VERSION BF578188.1 GI:11651900
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 691)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LLM9774 row: e column: 23
High quality sequence stop: 690.
Location/Qualifiers

FEATURES
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1. 594
/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3489635"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_1lb="NCI CGAP Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI; Site:2: NotI. Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

FEATURES
source
1. 691
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4209022"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NCI CGAP Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: SalI. Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

ORIGIN
Query Match 39.3%; Score 280.8; DB 2; Length 594;
Best Local Similarity 92.3%; Pred. No. 9,4e-71;
Matches 310; Conservative 0; Mismatches 17; Indels 9; Gaps 1;
QY 1 AGTATTGTGATGACCCAGACTCCCAATTCCTGCTGTATCAGACAGAGACAGGGTTACC 60
DB 47 AATGTTGTGATGACCCAGACTCCCAATTCCTGCTGTATCAGACAGAGACAGGGTTACC 106
QY 61 ATAACCTGCAAGGCCAGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 107 ATTAACCTGCAAGGCCAGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 166
QY 121 GGGCAGTCTCCGAACTGCTGATATCTGTCATCCCAATGCTTACCTGATGATGATGATGATGAT 180
DB 167 GGGCAGTCTCCGAACTGCTGATATCTGTCATCCCAATGCTTACCTGATGATGATGATGATGAT 226
QY 181 CGCTTCACTGGCAGTGTATGGAACGATTTTCACTTTCACATCAGACCTGTGACAGGCT 240
DB 227 CGCTTCACTGGCAGTGTATGGAACGATTTTCACTTTCACATCAGACCTGTGACAGGCT 286
QY 241 GAAAGCCTGGCAGTGTATTTCTGTCAAGAGATTTAAGCT-----CGCTCGAGGG 291
DB 287 GAAAGCCTGGCAGTGTATTTCTGTCAAGAGATTTAAGCTCTCCGTACAGTTTCGAGGG 346
QY 292 GGAACCAAGCTGAAATTAAGTGGAGGGGCTTCA 327
DB 347 GGAACCAAGCTGAAATTAAGTGGAGGGGCTGATGCA 382

RESULT 6
LOCUS BF578188 691 bp mRNA linear EST 12-DEC-2000
DEFINITION 602094691.F1 NCI CGAP Co24 Mus musculus cDNA clone IMAGE:4209022 5',
ACCESSION mRNA sequence, BF578188

ORIGIN
Query Match 38.7%; Score 276; DB 2; Length 691;
Best Local Similarity 85.6%; Pred. No. 2.5e-69;
Matches 322; Conservative 0; Mismatches 45; Indels 9; Gaps 1;
QY 339 CTCTGGCGGTGGCGATCGCAGGTGAGTGAAGAGTCAAGACCTGGCTGGTGGCGCC 398
DB 54 CCCAAGCTGTGCCCTGTCCAGGTGACGTAAGAGTCAAGACCTGGCTGGTGGCGCC 113
QY 399 CTACAGAGCCTGTCCATCATCTGACCTGTCTGTGGTTTCACTTAACCAATTAATGATG 458
DB 114 CTCACAGACCTGTCCATCATCTGACCTGTCTGTGGTTTCACTTAACCAATTAATGATG 173
QY 459 ACACGTGGTGGCAGCTCCAGAAAGGCTCTGAGTGGCTGGAGTAAATATGAGCTGG 518
DB 174 AAGCTGGTGGCAGCTCCAGAAAGGCTCTGAGTGGCTGGAGTAAATATGAGCTGG 233
QY 519 TGGAGCACAAAATTAATTTGGCTCTTAATGTCAGACTGAGCATCAGACAGACAATCT 578
DB 234 TGGAGCACAAAATTAATTTAGCTCTCAATTCAGACTGAGCATCAGACAGACAATCT 293
QY 579 CAAGACCAAGTTTCTTTAAATGAACAGCTCTGCAAACTGATGAACAGCCATTAATGA 638
DB 294 CAAGATCAAGTTTCTTTAAATGAACAGCTCTGCAAACTGATGAACAGCCATTAATGA 353
QY 639 CTGTGCAAGTCGGGGGGGTAACTACAGGCTATGCTTGAATCTAGTGGGTCAAGAACTCT 698
DB 354 CTGTGCA-----GAAATGCACTGGGACTTTGACTTGGGGCCCAAGGCAACAC 404
QY 699 AGTCAACGTCTCTCTCA 714
DB 405 TCTCAACGTCTCTCTCA 420

RESULT 7
LOCUS BQ940476 970 bp mRNA linear EST 21-AUG-2002
DEFINITION BQ940476 AGENCOURT_8879458 NCI CGAP Co24 Mus musculus cDNA clone

IMAGE:6475820 5', mRNA sequence.
B0940476 GI:22355954
EST.
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 970)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgarbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
Plate: LLM14015 row: c column: 21
High quality sequence start: 3
High quality sequence stop: 415.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6475820"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-Sport6; Site: 1; NotI; Site 2: SalI; Cloned unidirectionally. Primer: oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP library."
ORIGIN
Query Match 37.2%; Score 265.4; DB 5; Length 970;
Best Local Similarity 83.1%; Pred. No. 3.5e-66;
Matches 315; Conservative 0; Mismatches 61; Indels 3; Gaps 1;
QY 339 CTCGCGCGGTGGCGATGCGAGGTGAAGAGTCAGACCTGGCTGTGGCGCC 398
DB 54 CCCAAGCTGTCTCTGCCAGGTGCACTGAAGAGACAGACCTGGCTGTGGCGCC 113
QY 399 CTCACAGAGCTGTCCATCTTGACATGCTCTGGGTTTCATTAAACAATTATGGTGT 458
DB 114 CTCACAGAGCTGTCCATCTTGACATGCTCTGGGTTTCATTAAACAATTATGGTGT 173
QY 459 ACACTGGGTTGCGCAGCTCCAGGAAAGGCTCTGGAGTGGGAGTAAATATGGGCTGG 518
DB 174 CCACCTGGGTTGCGCAGCTCCAGGAAAGGCTCTGGAGTGGGAGTAAATATGGGAGTA 233
QY 519 TGAAGACCAATTAATTTGGCTTTATGTCCAGTGAATGACAGCAAGCAACTC 578
DB 234 TGAAGACCAATTAATTTGGCTTTATGTCCAGTGAATGACAGCAAGCAACTC 293
QY 579 CAAGAGCAGGTTTCTTAAATGAACAGTCTGAATCTGATGACAGCATGTACTA 638
DB 294 CAAGAGCAGGTTTCTTAAATGAACAGTCTGAATCTGATGACAGCATGTACTA 353
QY 639 CTGTGCGAGTGGGG--GGGTAATACGCTATGCTTTGGACTACTGGGGTCAAGAAC 695
DB 354 CTGTGCGAGTGGGGTGAAGGCGGCTTAACAATTTGCTTAATGCGGCCCAAGGAC 413
QY 696 CTGAGTCAAGCTCTCTCTA 714
DB 414 TCTGTACTGTCTCTGCA 432
RESULT 8

CR047446/c
LOCUS CR047446 831 bp DNA linear GSS 05-JUN-2004
DEFINITION Forward strand read from insert in 5'HRT insertion targeting and chromosome engineering clone MHPN40c19, genomic survey sequence.
ACCESSION CR047446
VERSION CR047446.1 GI:49780504
KEYWORDS GSS; genome survey sequence; MGCER.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 831)
ADAMS, D.J., BIGGS, P.J., COX, A.V., DAVIES, R.M., VAN DER WEYDEN, L., JONKERS, J., SMITH, J., PLUMB, R.W., TAYLOR, R.G., NIEHJIM, I., YU, Y., ROGERS, J., and BRADLEY, A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. <http://www.sanger.ac.uk/MICER>
Location/Qualifiers
1..831
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN40c19"
/clone_lib="MHPN"
ORIGIN
Query Match 36.8%; Score 262.4; DB 9; Length 831;
Best Local Similarity 91.4%; Pred. No. 2.5e-65;
Matches 278; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 346 GGTGGCGGATGCGAGGTGCGAGTGAAGAGTCAAGAGCTGGCCGTGGCCCTCAG 405
DB 327 GGTGTCTGTCTCCAGGTGCGAGTGAAGAGTCAAGAGCTGGCCCTCAG 268
QY 406 AGCTGTCCATCACTTCACTGCTCTGGGTTTCATTAAACAATTATGGTGTACACTGG 465
DB 267 AGCTGTCCATCACTTCACTGCTCTGGGTTTCATTAAACAATTATGGTGTACACTGG 208
QY 466 GTTGGCAGCTCCAGGAAAGGCTGTGAGTGGCTGGAAGTAAATATATGGCTGTGAAGC 525
DB 207 GTTGGCAGCTCCAGGAAAGGCTGTGAGTGGCTGGAAGTAAATATATGGCTGTGAAGC 148
QY 526 ACAATTAATTAATTTGGCTTTATGTCCAGTGAATGACAGCAAGCAACTCCAAAGC 585
DB 147 ACAATTAATTAATTTGGCTTTATGTCCAGTGAATGACAGCAAGCAACTCCAAAGC 88
QY 586 CAAATTTCTTAAATGAACAGTCTGAATCTGATGACAGGCAATGACTACTGTGCC 645
DB 87 CAAATTTCTTAAATGAACAGTCTGAATCTGATGACAGGCAATGACTACTGTGCC 28
QY 646 AGTC 649
DB 27 AGAC 24
RESULT 9
LOCUS BF579344 930 bp mRNA linear EST 12-DEC-2000
DEFINITION 60209563.F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4215751 5', mRNA sequence.
ACCESSION BF579344
VERSION BF579344.1 GI:11653056
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 930)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM9791 row: n column: 08
High quality sequence stop: 633.

FEATURES

source

Location/Qualifiers
1. .930
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4215751"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Colon; Vector: PCMV-SPORE; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP library."

ORIGIN

Query Match 36.8%; Score 262.4; DB 2; Length 930;
Best Local Similarity 83.0%; Pred. No. 2.6e-65;
Matches 312; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

QY 339 CTCTGGCGGTGGGCGATCCGAGTGCAGTGAAGAAGTCAAGACCTGGCTGGTGGCC 398
DB 56 CCCAGACTGTCTCTCTCCAGGTGACGCTGAAGAGACAGGACCTGGCTGGTGGCC 115
QY 399 CTCAGAGGCTGTGCATCATCTTGCACCTGCTCTGGTTTCTTAACCAATATAGTGT 458
DB 116 CTCACAGAGCTGTCCATCATCATGACCGCTCAGGATTCCTATTAACCAAGCTATGTAT 175
QY 459 ACACTGGGTTCGCGACCTCCAGAAAGGTCTGAGTGGCTGGAGTAATATGGCTGG 518
DB 176 ACATGATTCGCGACGCTCCAGGAAAGGTCTGGAGTGGCTGGAGTATTTGGAGTGA 235
QY 519 TGGAGCACAATTAATTTGGCTTTATGTCACAGCTGAGCATACAGCAAGCAACTC 578
DB 236 TGGGAACACAAATTAATTTCACTTCAATCAATCAATGAGCATACAGCAAGCAACTC 295
QY 579 CAGAGCCAGTTTCTTAATAATGAACAGTGCACAACTGATGACAGCCCAATGACTA 638
DB 296 CAGAGCCAGTTTCTTAATAATGAATGCTCCAACTGATGACAGCCCAATGACTA 355
QY 639 CTGTGCGAGTGGGGGCTTAACCTACCGCTATGCTTTGACTACTGGGGTCAAGAACTC 698
DB 356 CTGTGCGAGCAATGGGG---ATTACCTTAATTAATGACTACTGGGGTCAAGAACTC 412
QY 699 AGTCACCGTCTCTCA 714
DB 413 AATCACCGTCTCTCA 428

RESULT 10

LOCUS COS67792 792 bp mRNA linear EST 19-JUL-2004
DEFINITION AGENCOURT 28626487 NIH_MGC_249 Rattus norvegicus cDNA clone
IMAGE:7379450 5', mRNA sequence.

ACCESSION COS67792
VERSION COS67792.1 GI:50380421

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 792)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE
JOURNAL
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM15536 row: f column: 24
High quality sequence start: 15
High quality sequence stop: 703.

FEATURES

source

Location/Qualifiers
1. .792
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7379450"
/lab_host="DH10B TONa"
/note="Organ: spleen; Vector: pExpress-1; Site 1: EcoRV;
Site 2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (TRI-reagent method). CDNA
was primed using oligo-dr primer:
5'-pactgtgtctgtagtcgcagcgccgccc(7)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.4 kb. This primary
library is normalized (primary library is NIH_MGC_248)
and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH_MGC library"

ORIGIN

Query Match 36.3%; Score 259; DB 7; Length 792;
Best Local Similarity 81.1%; Pred. No. 2.5e-64;
Matches 301; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 344 GCGGTGGCGATGCGAGTGCAGTGAAGAAGTCAAGACCTGGCTGGTGGCCCTCAC 403
DB 86 GCTGTCTCTGTCCAGGTGACGCTGAAGAGTCAAGACTGTCTGGTGCAGCCCTCAC 145
QY 404 AAGCCTGTTCATCACTTCACTGTCTCTGGTTTCAATTAACAATTAATGTGTAACCT 463
DB 146 AGACCTGTTCCTCACTGCTGCTGATTCATTAATGACTACAGTGAACACT 205
QY 464 GGGTTCGCGAGCTCCAGAAAGGTCTGAGTGGCTGGAGTAATATGGCTGTGAA 523
DB 206 GGGTTCGCGAGCTCCAGAAAGGTCTGAGTGGAGTAATGAATGATGAGGAG 265
QY 524 GCACAAATTAATTTGCGCTTTATGTCAGACTGAGCATACAGCAAGCAACTCCAAG 583
DB 266 ACACATTAATTAATTTGAGCTTCAATATCCGACTGAGCATACAGAGGACACTCCAAG 325
QY 584 GCCAAGTTTCTTAATAATGAACAGTGCACAACTGATGACACAGGCATGTACTATG 643
DB 326 ACCAAGTTTCTTAATAATGAACAGTGCACAACTGATGACACAGGCATTTACTATGTA 385
QY 644 CCAGTGGGGGGGTAACTACGCGCTATGCTTTGACTACTGGGTGAAGAACTCACTG 703
DB 386 CCAGAGCACCGGATTAACAGTGTGACTTGTGATTAATCGGGCCAAAGAGTCATG 445
QY 704 CCGTCTCTCA 714
DB 446 CAGTCTCTCA 456

RESULT 11

COS74382
LOCUS COS74382 793 bp mRNA linear EST 19-JUL-2004
DEFINITION AGENCOURT 28451299 NIH_MGC_248 Rattus norvegicus cDNA clone
IMAGE:736659 5', mRNA sequence.
ACCESSION COS74382
VERSION COS74382.1 GI:50387011
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 793)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@bbs-rt@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM15503 row: b column: 01
High quality sequence start: 46
High quality sequence stop: 699.
Location/Qualifiers
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/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:736659"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_248"
/note="Organ: spleen; Vector: pExpress-1; Site_1: EcoRV;
Site_2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (TRI-reagent method). cDNA
was primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGGAGCGGCCCT(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.7 kb. This is a
primary library (normalized library is NIH_MGC_249) and
was constructed by Open Biosystems. Note: this is a NIH_MGC
library"
ORIGIN
Query Match 36.1%; Score 257.4; DB 7; Length 793;
Best Local Similarity 80.9%; Pred. No. 7.3e-64;
Matches 300; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
QY 344 GCGGTGGCGATCGAGGTGAAGAAGTCAAGCTGGCTGTGGCGCCCTCAG 403
DB 94 GCTGTGCTCTCCAGGTGAGTGAAGAGTCAAGCTGGCTGTGGCGCCCTCAG 153
QY 404 AGAGCCGTGCATCACTGCTGCTGGGTTTCAATTAACCAATATAGTGAACCT 463
DB 154 AGACCCGTGCTCCAGTCACTGCTGTGGGTTTCAATTAACCAATATAGTGAACCT 213
QY 464 GGGTTCGACAGCTTCAGAAAGGCTGAGTGGCTGGAGTAATATGGCTGGTGA 523
DB 214 GGGTTCGACAGCTTCAGAAAGGCTGAGTGGATGAGTATCTGAGTGGTGA 273
QY 524 GCACAAATTAATTTGGCTCTTATGTCAGACTGAGATCAAGCAAGCAACTTCAGA 583
DB 274 ACACAGATTAATTAATTTGGCTCTTATGTCAGACTGAGATCAAGCAAGCAACTTCAGA 313

QY 584 GCCAAGTTTCTTAAAAATGACAGTCTGCACAACTGATGACAGCCATGTAAGTCTGTG 643
DB 334 GCCAAGTTTCTTAAACATGAAAGTCTGCACAACTGATGACAGCCATGTAAGTCTGTG 393
QY 644 CCAAGTGGGGGGGTAAGTCAAGCTGCTTGTGACTACTGGGGTCAAGAACTTCAGTCA 703
DB 394 ACAGAAATGGCCCTACTACGAGAGGTTGTGCTTACTGGGGCCAAAGGCACTGTGTCA 453
QY 704 CCGTCTCTCA 714
DB 454 CTGTCCTTCA 464
RESULT 12
LOCUS COS58560 914 bp mRNA linear EST 19-JUL-2004
DEFINITION AGENCOURT 28542576 NIH_MGC_248 Rattus norvegicus cDNA clone
IMAGE:7374685 5', mRNA sequence.
ACCESSION COS58560
VERSION COS58560.1 GI:50371156
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 914)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@bbs-rt@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM15523 row: p column: 11
High quality sequence start: 23
High quality sequence stop: 708.
Location/Qualifiers
1..914
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7374685"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_248"
/note="Organ: spleen; Vector: pExpress-1; Site_1: EcoRV;
Site_2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (TRI-reagent method). cDNA
was primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGGAGCGGCCCT(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.7 kb. This is a
primary library (normalized library is NIH_MGC_249) and
was constructed by Open Biosystems. Note: this is a NIH_MGC
library"
ORIGIN
Query Match 35.4%; Score 253; DB 7; Length 914;
Best Local Similarity 82.2%; Pred. No. 1.5e-62;
Matches 305; Conservative 0; Mismatches 60; Indels 6; Gaps 1;
QY 344 GCGGTGGCGATCGAGGTGAAGAAGTCAAGCTGGCTGTGGCGCCCTCAG 403

Db 94 GCTGTGCTCTGTCCAGAGTCAGCTGAGAGTCAAGGACCTGGCTGTGTCAGCCCTCAG 153
QY 404 AGAGCCGTGCATCAGTTCGACGTCTCTGGGTTTTCATTAAACCAATTATGTTGTCACCT 463
Db 154 AGACCCGTGCTCCTCAGCTGCTGTCTGTGGTTCTCTACTAACCAAGTATGTGTAACT 213
QY 464 GGGTTCGCGACCTCCAGAAAAGGTCGTGAGTGGCTGAGATTAATATGCTGTGGAA 523
Db 214 GGGTTCGCGACCTCCAGAAAAGGTCGTGAGTGGAGTGAACAATATGATGAGGAA 273
QY 524 GCACAATTAATATGCTGTCTTATGTCTCAGACTGAGCATCAGCAAGACAATCTCCAGA 583
Db 274 GCACAGATTCAATTCAGTCTCTCAAAATCCGACTGAGCATCAGAGGACACTTCTAAGA 333
QY 584 GCCAAGTTTCTTAAATAAGACAGTCTGCAACTGATGACAGCCATGACTACCTGTG 643
Db 334 GCCAAGTTTCTTAAATAAGACAGTCTGCAACTGATGACAGCCATGACTACCTGTG 393
QY 644 CCAAGTCGGGGGGGTAACGCTATGCTTTGCACTAGGCTCAAGAACTCAGTCA 703
Db 394 CCA-----GAGAACTACTACAGTGTACTTGTATTTCTGGGCGCAAGAGTCAATGTCA 447
QY 704 CCGTCTCTCA 714
Db 448 CAGTCTCTCA 458

RESULT 13
BF580610 883 bp mRNA linear EST 12-DEC-2000
LOCUS 602093730F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4208022 5',
DEFINITION mRNA sequence.
ACCESSION BF580610 GI:11654322
VERSION EST.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus (house mouse)
REFERENCE 1 (bases 1 to 883)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
DNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL9771 row: 1 column: 07
High quality sequence stop: 639.
Location/Qualifiers
1. 883
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4208022"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: PCMV-SPORE6; Site: 1; NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

FEATURES
source
1. 883
Location/Qualifiers

ORIGIN

Query Match 35.1%; Score 250.4; DB 2; Length 883;
Best Local Similarity 90.5%; Pred. No. 8.4e-62;
Matches 304; Conservative 0; Mismatches 21; Indels 11; Gaps 3;

QY 1 AGTATTGTGATGACCCAGACGATCCCAATTCTGTTGTATCAGACGAGACAGGTTACC 60
Db 72 ATTATTTTATGATACCCAGACGATCCCAATTCTGCG- TGTATCAGCAGGAGACAGGGTTACC 130
QY 61 ATTAACCTGCAAGCCAGTGAAGTGTGATATGATATGTGGCTTTGGTACCAAGAACCA 120
Db 131 ATTAACCTGCAAGCCAGTGAAGTGTGATATGATATGATATGATATGATATGATATGAT 189
QY 121 GGGCAGTCTCCGAAACTGTGATATATCTGTGATCCATCGCTACACTGAGTCCCTGAT 180
Db 190 GGGCAGTCTCTTAACTGTGATATATCTGATATGATATGATATGATATGATATGATATGAT 249
QY 181 CGGTTCACTGGCAGTGTATATGATATGATATGATATGATATGATATGATATGATATGAT 240
Db 250 CGGTTCACTGGCAGTGTATATGATATGATATGATATGATATGATATGATATGATATGAT 309
QY 241 GAAGACCTGGCAGTGTATATGATATGATATGATATGATATGATATGATATGATATGAT 291
Db 310 GAAGACCTGGCAGTGTATATGATATGATATGATATGATATGATATGATATGATATGAT 369
QY 292 GGGACCAAGCTGGAATTAAGTGTGAGGCGGTTCA 327
Db 370 GGCACCAAGCTGGAATTAAGTGTGAGGCGGTTCA 405

RESULT 14
BU522894 912 bp mRNA linear EST 13-SEP-2002
LOCUS BU522894
DEFINITION AGENCOURT_10158089 NCI_CGAP_Co24 Mus musculus cDNA clone
IMAGE:6529489 5', mRNA sequence.
ACCESSION BU522894
VERSION BU522894.1 GI:22833332
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)
REFERENCE 1 (bases 1 to 912)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
DNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL4129 row: 1 column: 01
High quality sequence stop: 653.
Location/Qualifiers
1. 912
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/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6529489"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: PCMV-SPORE6; Site: 1; NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

FEATURES
source
1. 912
Location/Qualifiers

ORIGIN

Query Match 35.0%; Score 250; DB 5; Length 912;
Best Local Similarity 81.1%; Pred. No. 1.1e-61;
Matches 305; Conservative 0; Mismatches 65; Indels 6; Gaps 1;
QY 339 CTCTGCGGTGCGGATTCGAGGTGCAAGTCAAGACGACCTGGCTGTGCGGCC 398

Db	35	CCAAAGCTGTGTCTTATCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	94
Qy	339	CTCAGAGGCTGTGTCTTATCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	458
Db	95	CTCAGAGGCTGTGTCTTATCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	154
Qy	459	ACACTGGGTTGCGGCTCTCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	518
Db	155	ACACTGGGTTGCGGCTCTCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	214
Qy	519	TGGAAGCACAATTAATTAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTC	578
Db	215	TGGAAGCACAAGCTATTAATTAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTC	274
Qy	579	CAAGAGCCAGTTTCTTTAAATGAACAGTCTGCAAACTGATGACACAGCATCTACTA	638
Db	275	CAAGAGCCAGTTTCTTTAAATGAACAGTCTGCAAACTGATGACACAGCATCTACTA	334
Qy	639	CTGTGCCAGTGGGGGGGTAAGTACGCTATGCTTGGACTACTGATGACAGCAAGCAACTC	698
Db	335	CTGTGTCTA-----GAAATTAATCTACGCTGCTGTAATTGATGCTTGGGGCGGAGCAAC	388
Qy	699	AdTCACCGTCTCTCTCA	714
Db	389	GGTACCGCTCTCTCTCA	404
RESULT 15			
LOCUS	BY733751	664 bp	mRNA linear EST 17-DEC-2002
DEFINITION	BY733751 RIKEN full-length enriched, adult male accessory axillary lymph node Mus musculus cDNA clone G630076H03 5', mRNA sequence.		
ACCESSION	BY733751		
VERSION	BY733751.1	GI:27146878	
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 664)		
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nishida, I., Otsu, N., Saito, R., Suzuki, H., Yamana, K., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schindbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisler, K. W., Blake, J. A., Bradt, D., Bruscia, V., Chochia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gaitanaris, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gueniche, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawauchi, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Kongaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pereira, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramchandran, S., Raveill, T., Reed, J. C., Reed, D. O., Reid, J., Ring, B. E., Ringwald, M., Sander, A. S., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wamboldt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyman, B. O., Yang, A., Yang, I., Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayashida, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Aizawa, T., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohata, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.		

Qy	339	CTCAGAGGCTGTGTCTTATCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	398
Db	70	CCAAAGCTGTGTCTTATCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	129
Qy	339	CTCAGAGGCTGTGTCTTATCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	458
Db	130	CTCAGAGGCTGTGTCTTATCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	189
Qy	459	ACACTGGGTTGCGGCTCTCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	518
Db	190	ACACTGGGTTGCGGCTCTCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	249
Qy	519	TGGAAGCACAATTAATTAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTC	578
Db	250	TGGAAGCACAAGCTATTAATTAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTC	309
Qy	579	CAAGAGCCAGTTTCTTTAAATGAACAGTCTGCAAACTGATGACACAGCATCTACTA	638
Db	310	CAAGAGCCAGTTTCTTTAAATGAACAGTCTGCAAACTGATGACACAGCATCTACTA	369
Qy	639	CTGTGCCAGTGGGGGGGTAAGTACGCTATGCTTGGACTACTGATGACAGCAAGCAACTC	698

FEATURES			
source			
1..664			
/organism="Mus musculus"			
/mol_type="mRNA"			
/strain="C57BL/6J"			
/db_xref="taxon:10090"			
/clone="G630076H03"			
/sex="male"			
/tissue_type="accessory axillary lymph node"			
/dev_stage="adult"			
/clone_lib="RIKEN full-length enriched, adult male accessory axillary lymph node"			
ORIGIN			
Query Match	34.6%;	Score 247;	DB 6; Length 664;
Best Local Similarity	79.5%;	Pred. No. 7.7e-61;	
Matches 311;	Conservative	0; Mismatches 65;	Indels 15; Gaps 1;

Qy	339	CTCAGAGGCTGTGTCTTATCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	398
Db	70	CCAAAGCTGTGTCTTATCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	129
Qy	339	CTCAGAGGCTGTGTCTTATCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	458
Db	130	CTCAGAGGCTGTGTCTTATCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	189
Qy	459	ACACTGGGTTGCGGCTCTCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	518
Db	190	ACACTGGGTTGCGGCTCTCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	249
Qy	519	TGGAAGCACAATTAATTAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTC	578
Db	250	TGGAAGCACAAGCTATTAATTAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTC	309
Qy	579	CAAGAGCCAGTTTCTTTAAATGAACAGTCTGCAAACTGATGACACAGCATCTACTA	638
Db	310	CAAGAGCCAGTTTCTTTAAATGAACAGTCTGCAAACTGATGACACAGCATCTACTA	369
Qy	639	CTGTGCCAGTGGGGGGGTAAGTACGCTATGCTTGGACTACTGATGACAGCAAGCAACTC	698

Qy	339	CTCAGAGGCTGTGTCTTATCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	398
Db	70	CCAAAGCTGTGTCTTATCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	129
Qy	339	CTCAGAGGCTGTGTCTTATCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	458
Db	130	CTCAGAGGCTGTGTCTTATCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	189
Qy	459	ACACTGGGTTGCGGCTCTCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	518
Db	190	ACACTGGGTTGCGGCTCTCCAGAGTGAGTGAAGCATGACGCTCTGGGCTAGTGCACC	249
Qy	519	TGGAAGCACAATTAATTAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTC	578
Db	250	TGGAAGCACAAGCTATTAATTAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTC	309
Qy	579	CAAGAGCCAGTTTCTTTAAATGAACAGTCTGCAAACTGATGACACAGCATCTACTA	638
Db	310	CAAGAGCCAGTTTCTTTAAATGAACAGTCTGCAAACTGATGACACAGCATCTACTA	369
Qy	639	CTGTGCCAGTGGGGGGGTAAGTACGCTATGCTTGGACTACTGATGACAGCAAGCAACTC	698

Db 370 CTGTGCCAAAATGGGTATGAGAGGATTACGACGGAGACGTACTTGTGACTACTG 429
Qy 684 GGGTCAAGGAACCTCAGTCACCGTCTCCTCA 714
Db 430 GGGCAAGGCACTCTCAAGTCTCTCA 460

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